

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

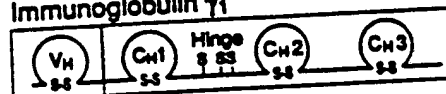
B35

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

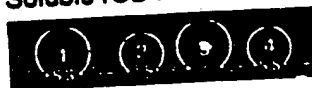
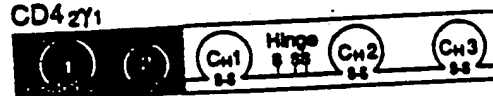
(51) International Patent Classification ⁴ : C12N 15/00, C12P 21/02 A61K 37/02 // G01N 33/566		A1	(11) International Publication Number: WO 89/02922 (43) International Publication Date: 6 April 1989 (06.04.89)
(21) International Application Number: PCT/US88/03414 (22) International Filing Date: 3 October 1988 (03.10.88)		(74) Agents: HENSLEY, Max, D. et al.: Genentech, Inc., Legal Department, 460 Point San Bruno Boulevard, South San Francisco, CA 94080 (US).	
(31) Priority Application Numbers: 104,329 Not furnished		(81) Designated States: AT (European patent), AU, BE (Eu- ropean patent), CH (European patent), DE (Euro- pean patent), DK, FR (European patent), GB (Euro- pean patent), IT (European patent), JP, LU (Euro- pean patent), NL (European patent), NO, SE (Euro- pean patent).	
(32) Priority Dates: 2 October 1987 (02.10.87) 28 September 1988 (28.09.88)		Published With international search report.	
(33) Priority Country: US			
(71) Applicant: GENENTECH, INC. [US/US]: 460 Point San Bruno Boulevard, South San Francisco, CA 94080 (US).			
(72) Inventors: CAPON, Daniel, J.: 817 Oregon Avenue, San Mateo, CA 94402 (US). GREGORY, Timothy, J.: 414 Pinehill Road, Hillsborough, CA 94010 (US).			

(54) Title: ADHESION VARIANTS

CD4

Immunoglobulin γ_1 

Soluble rCD4

CD4 γ_1 CD4 γ_1 

(57) Abstract

Novel derivatives of cell surface proteins which are homologous to the immunoglobulin superfamily (adhesions) are provided. Amino acid sequence variations are introduced into adhesion, the most noteworthy of which are those in which the transmembrane and, preferably, cytoplasmic domains are rendered functionally inactive, and in which adhesion extracellular domains replace an immunoglobulin variable region. These variants are useful in therapy or diagnostics, in particular, CD4 variants are therapeutically useful in the treatment of HIV infections.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AT	Austria	FR	France	ML	Mali
AU	Australia	GA	Gabon	MR	Mauritania
BB	Barbados	GB	United Kingdom	MY	Malawi
BE	Belgium	HU	Hungary	NL	Netherlands
BG	Bulgaria	IT	Italy	NO	Norway
BJ	Benin	JP	Japan	RO	Romania
BR	Brazil	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic	KR	Republic of Korea	SE	Sweden
CG	Congo	LI	Liechtenstein	SN	Senegal
CH	Switzerland	LE	Sri Lanka	SU	Soviet Union
CM	Cameroun	LU	Luxembourg	TD	Chad
DE	Germany, Federal Republic of	MC	Monaco	TG	Togo
DK	Denmark	MG	Madagascar	US	United States of America
FI	Finland				

ADHESION VARIANTS

Background of the Invention

5 This application relates to compositions for antiviral or immunomodulatory therapy. In particular, it relates to compositions useful in the treatment of Human Immunodeficiency Virus (HIV) infections.

10 The primary immunologic abnormality resulting from infection by HIV is the progressive depletion and functional impairment of T lymphocytes expressing the CD4 cell surface glycoprotein (H. Lane et al., Ann. Rev. Immunol. 3:477 [1985]). CD4 is a non-polymorphic glycoprotein with homology to the immunoglobulin gene superfamily (P. Maddon et al., Cell 42:93
15 [1985]). Together with the CD8 surface antigen, CD4 defines two distinct subsets of mature peripheral T cells (E. Reinherz et al., Cell 19:821 [1980]), which are distinguished by their ability to interact with nominal antigen targets in the context of class I and class II major histocompatibility complex (MHC) antigens, respectively (S. Swain, Proc. Natl. Acad. Sci. 78:7101 [1981]; E. Engleman et al., J. Immunol. 127:2124 [1981]; H. Spitz et al., J. Immunol. 129:1563 [1982]; W. Biddison et al., J. Exp. Med. 156:1065
20 [1982]; and D. Wilde et al., J. Immunol. 131:2178 [1983]). For the most part, CD4 T cells display the helper/inducer T cell phenotype (E. Reinherz, supra), although CD4 T cells characterized as cytotoxic/suppressor T cells have also been identified (Y. Thomas et al., J. Exp. Med. 154:459 [1981]; S. Meuer et al., Proc. Natl. Acad. Sci. USA 79:4395 [1982]; and A. Krensky et al., Proc. Natl. Acad. Sci. USA 79:2365 [1982]). The loss of CD4 helper/inducer T
25 cell function probably underlies the profound defects in cellular and humoral immunity leading to the opportunistic infections and malignancies characteristic of the acquired immunodeficiency syndrome (AIDS) (H. Lane supra).

9
2

-2-

Studies of HIV-I infection of fractionated CD4 and CD8 T cells from normal donors and AIDS patients have revealed that depletion of CD4 T cells results from the ability of HIV-I to selectively infect, replicate in, and ultimately destroy this T lymphocyte subset (D. Klatzmann et al., Science 225:59 [1984]). The possibility that CD4 itself is an essential component of the cellular receptor for HIV-I was first indicated by the observation that monoclonal antibodies directed against CD4 block HIV-I infection and syncytia induction (A. Dalgleish et al., Nature [London] 312:767 [1984]; J. McDougal et al., J. Immunol. 135:3151 [1985]). This hypothesis has been confirmed by the demonstration that a molecular complex forms between CD4 and gp120, the major envelope glycoprotein of HIV-I (J. McDougal et al., Science 231:382 [1986]; and the finding that HIV-I tropism can be conferred upon ordinarily non-permissive human cells following the stable expression of a CD4 cDNA (P. Maddon et al., Cell 47:333 [1986]). Furthermore, the neurotropic properties of HIV-I, reflected by a high incidence of central nervous system dysfunction in HIV-I infected individuals (W. Snider et al., Ann. Neurol. 14:403 [1983]), and the ability to detect HIV-I in the brain tissue and cerebrospinal fluid of AIDS patients (G. Shaw et al., Science 227:177 [1985]; L. Epstein, AIDS Res. 1:447 [1985]; S. Koenig, Science 233:1089 [1986]; D. Ho et al., N. Engl. J. Med. 313:1498 [1985]; J. Levy et al., Lancet II:586 [1985]), appears to have its explanation in the expression of CD4 in cells of neuronal, glial and monocyte/macrophage origin (P. Maddon, Cell 47:444 [1986]; I. Funke et al., J. Exp. Med. 165:1230 [1986]; B. Tourville et al., Science 234:610 [1986]).

In addition to determining the susceptibility to HIV-I infection, the manifestation of cytopathic effects in the infected host cell appears to involve CD4. Antibody to CD4 was found to inhibit the fusion of uninfected CD4 T cells with HIV-I infected cells in vitro; moreover, the giant multinucleated cells produced by this event die shortly after being formed resulting in the

depletion of the population of CD4 cells (J. Lifson *et al.*, Science 232:1123 [1986]). Formation of syncytia also requires gp120 expression, and can be elicited by coculturing CD4-positive cell lines with cell lines expressing the HIV-I *env* gene in the absence of other viral structural or regulatory proteins (J. Sodroski *et al.*, Nature 322:470 [1986]; J. Lifson *et al.*, Nature 323:725 [1986]). Thus, in mediating both the initial infection by HIV-I as well as eventual cell death, the interaction between gp120 and CD4 constitutes one of several critical entry points in the viral life cycle amenable to therapeutic intervention (H. Mitsuya *et al.*, Nature 325:773 [1987]).

The known sequence of the CD4 precursor predicts a hydrophobic signal peptide, an extracellular region of approximately 370 amino acids, a highly hydrophobic stretch with significant identity to the membrane-spanning domain of the class II MHC beta chain, and a highly charged intracellular sequence of 40 residues (P. Madden, Cell 42:93 [1985]). The extracellular domain of CD4 consists of four contiguous regions each having amino acid and structural similarity to the variable and joining (V-J) domains of immunoglobulin light chains as well as related regions in other members of the immunoglobulin gene superfamily (a subclass of which are defined herein by the coined term "adhesions". These structurally similar regions of CD4 are termed the V₁, V₂, V₃ and V₄ domains (denominated 1-4 in Fig. 3).

A successful strategy in the development of drugs for the treatment of many receptor mediated abnormalities has been the identification of antagonists which block binding of the natural ligand. Since the CD4 adhesion ordinarily binds to the recognition sites of the HIV envelope it would appear to be a candidate for therapeutically sequestering these HIV sites, thereby blocking viral infectivity. However, full length CD4 and other adhesions are cell membrane proteins which are anchored in the lipid bilayer of cells. The presence of membrane components will be undesirable

-4-

from the standpoint of manufacturing and purification. In addition, since adhesions are normally present only on cell surfaces, it would be desirable to produce adhesions in a form which is more stable in the circulation. Additionally, even truncated, soluble CD4 adhesion (generally referred to as CD4T) may not be optimally effective as a therapeutic since it possesses a relatively short biological half-life, binds to HIV no better than cell surface CD4, may not cross the placental or other biological barriers and since it merely sequesters the HIV recognition sites without in itself bearing an infected-cell killing or virus killing functionality.

Accordingly, it is an object of this invention to produce soluble, secreted adhesions. It is another object to produce CD4 derivatives useful in the treatment of AIDS and related conditions, in a manner essentially unaffected by the extreme degree of genetic variation observed among various HIV-I isolates and their respective env polypeptides (J.Coffin, Cell 46:1 [1986]). Still another object is to prepare adhesions fused to other polypeptides in order to provide molecules with novel functionalities such as those described above for therapeutic use, or diagnostic reagents for the *in vitro* assay of adhesions or their ligands. In particular, it is an objective to prepare molecules for directing toxins or effector molecules (for example the Fc domain of immunoglobulin) to cells bearing receptors for the adhesions, e.g. HIV gp120 in the case of CD4, and for use in facilitating purification of the adhesions. It is a further object to provide stable, highly purified adhesion preparations.

Summary

The objects of this invention are accomplished by providing nucleic acid encoding an amino acid sequence variant of an adhesion, in particular a variant in which the trans-membrane domain is modified so that it is no longer capable of becoming lodged in the

-5-

cell membrane. In the case of CD4 such variants are termed soluble CD4.

5 Variant adhesions are produced by a method comprising (a) transforming a host cell with nucleic acid encoding an amino acid sequence variant of an adhesion, (b) culturing the host cell and (c) recovering the variant adhesion from the host cell culture media or from lysates of the host cell.

10 In specific embodiments, the objects of this invention are accomplished by providing an adhesion variant selected from the group consisting of (a) an adhesion amino acid sequence variant having an inactivated transmembrane domain and (b) a polypeptide comprising an adhesion extracellular domain fused to the sequence of
15 a polypeptide which is different from the adhesion, this latter, for example, selected from a cytotoxin, an immunogen or a protein with a long plasma half life such as an immunoglobulin constant domain.

20 In a preferred embodiment a polypeptide comprising a gp120 binding domain of the CD4 adhesion is fused at its C-terminus to an immunoglobulin constant domain, or is linked to a cytotoxic polypeptide such as ricin.

25 The CD4 adhesion variants provided herein are purified and formulated in pharmacologically acceptable vehicles for administration to patients in need of antiviral, neuromodulatory or immunomodulatory therapy, in particular patients infected with HIV, and for use in the modulation of cell adhesion.

30 Brief Description of the Drawings

Figs. 1a-1c depict the amino acid and nucleotide sequence of a secreted form of the CD4 adhesion. The signal processing site is designated with an arrow.

WO 89/02922

-6-

Figs. 2a-2c depict the amino acid and nucleotide sequence of a fusion of the herpes gD leader and N-terminal 27 residues to the putative mature N-terminus of CD4T.

Fig. 3 depicts the structural elements of the native and soluble CD4 adhesion, the native human IgG₁ (γ₁) heavy chain and two exemplary heavy chain-CD4 chimeras.

Figs. 4a-4b are a map of the linked human IgG₁ (γ₁) chain fragment employed in the preparation of CD4 fusions. Insert sites are designated γ₁ and Fc.

Fig. 5 is a map of the human κ light chain fragment useful for CD4 fusions at the arrow flanked by V_κJ_κ (light variable and joining) and C_κ (light constant).

Detailed Description

Adhesions are cell surface polypeptides having an extracellular domain which is homologous to a member of the immunoglobulin gene superfamily, excluding, however, highly polymorphic members of this superfamily selected from the group of class I and class II major histocompatibility antigens, immunoglobulins and T-cell receptor α, β, γ and δ chains. Examples of adhesions include CD1, CD2, CD4, CD8, CD28, the γ, δ and ε chains of CD3, OX-2, Thy-1, the intercellular or neural cell adhesion molecules (I-CAM or N-CAM), lymphocyte function associated antigen-3 (LFA-3), neurocytoplasmic protein (NCP-3), poly-Ig receptor, myelin-associated glycoprotein (MAG), high affinity IgE receptor, the major glycoprotein of peripheral myelin (Po), platelet derived growth factor receptor, colony stimulating factor-1 receptor, macrophage Fc receptor, Fc gamma receptors and carcinoembryonic antigen. Homologous as defined herein means having the sequence of a member of the immunoglobulin gene superfamily or having a sequence therewithin which has substantially the same as (or a greater degree of) amino acid

-7-

sequence homology to a known member of the superfamily as the specific examples given above have to the sequence of an immunoglobulin variable or constant domain. Preferred adhesions are CD4, CD8 and high affinity IgE Fc receptor.

5 This invention is particularly concerned with amino acid sequence variants of adhesions. Amino acid sequence variants of adhesions are prepared with various objectives in mind, including increasing the affinity of the adhesion for its binding partner, 10 facilitating the stability, purification and preparation of the adhesion, increasing its plasma half life, improving therapeutic efficacy as described above in the background, introducing additional functionalities and lessening the severity or occurrence of side effects during therapeutic use of the adhesion. Amino acid 15 sequence variants of adhesions fall into one or a combination of the following classes: insertional, substitutional or deletional variants.

20 Insertional amino acid sequence variants are those in which one or more amino acid residues extraneous to the adhesion are introduced into a predetermined site in the adhesion including the C or N termini. Such variants are referred to as fusions of the adhesion and a different polypeptide. Such other polypeptides contain sequences other than those which are normally found in the 25 adhesion at the inserted position. Several groups of fusions are contemplated herein. Immunologically active adhesion fusions comprise an adhesion and a polypeptide containing a non-adhesion epitope. The non-adhesion epitope is any immunologically competent polypeptide, i.e., any polypeptide which is capable of eliciting an 30 immune response in the animal to which the fusion is to be administered or which is capable of being bound by an antibody raised against the non-adhesion polypeptide. Typical non-adhesion epitopes will be those which are borne by allergens, autoimmune epitopes, or other potent immunogens or antigens recognized by pre-existing antibodies in the fusion recipient, including bacterial 35

polypeptides such as trpLE, beta-galactosidase, viral polypeptides such as herpes gD protein, and the like. Immunogenic fusions are produced by cross-linking in vitro or by recombinant cell culture transformed with DNA encoding an immunogenic polypeptide. It is preferable that the immunogenic fusion be one in which the immunogenic sequence is joined to or inserted into the adhesion antigen or fragment thereof by a peptide bond(s). These products therefore consist of a linear polypeptide chain containing adhesion epitopes and at least one epitope foreign to the adhesion. It will be understood that it is within the scope of this invention to introduce the epitopes anywhere within the adhesion molecule or fragment thereof. Such fusions are conveniently made in recombinant host cells or by the use of bifunctional cross-linking agents. The use of a cross-linking agent to fuse the adhesion to the immunogenic polypeptide is not as desirable as a linear fusion because the cross-linked products are not as easily synthesized in structurally homogeneous form.

These immunogenic insertions are particularly useful when formulated into a pharmacologically acceptable carrier and administered to a subject in order to raise antibodies against the adhesion, which antibodies in turn are useful in diagnostics or in purification of adhesion by immunoaffinity techniques known per se. Alternatively, in the purification of adhesions, binding partners for the fused non-adhesion polypeptide, e.g. antibodies, receptors or ligands, are used to adsorb the fusion from impure admixtures, after which the fusion is eluted and, if desired, the adhesion is recovered from the fusion, e.g. by enzymatic cleavage.

Other fusions, which may or may not also be immunologically active, include fusions of the adhesion sequence with a signal sequence heterologous to the adhesion, fusions of transmembrane-modified CD4 adhesions, for example, to polypeptides having enhanced plasma half life (ordinarily >about 20 hours) such as immunoglobulin chains or fragments thereof, and fusions with

-9-

cytotoxic functionalities. Signal sequence fusions are employed in order to more expeditiously direct the secretion of the adhesion. The heterologous signal replaces the native adhesion signal, and when the resulting fusion is recognized, i.e. processed and cleaved by the host cell, the adhesion is secreted. Signals are selected based on the intended host cell, and may include bacterial yeast, mammalian and viral sequences. The herpes gD glycoprotein signal is suitable for use in mammalian expression systems.

Plasma proteins which have enhanced plasma half-life longer than that of transmembrane modified CD4 include serum albumin, immunoglobulins, apolipoproteins, and transferrin. Preferably, the adhesion-plasma protein fusion is not significantly immunogenic in the animal in which it is used and the plasma protein does not cause undesirable side effects in patients by virtue of its normal biological activity.

In a specific embodiment the adhesion immunoglobulin-like domain which may be homologous either to the constant or to the variable region domains is conjugated with an immunoglobulin constant region sequence. The resulting products are referred to herein as immunoadhesions. Immunoglobulins and certain variants thereof are known and many have been prepared in recombinant cell culture. For example, see U.S. Patent 4,745,055; EP 256,654; Faulkner et al., Nature 298:286 (1982); EP 120,694; EP 125,023; Morrison, J. Immun. 123:793 (1979); Köhler et al., P.N.A.S. USA 77:2197 (1980); Raso et al., Cancer Res. 41:2073 (1981); Morrison et al., Ann. Rev. Immunol. 2:23ⁿ (1984); Morrison, Science 229:1202 (1985); Morrison et al., P.N.A.S. USA 81:6851 (1984); EP 255,694; EP 266,663; and WO 88/03559. Reassorted immunoglobulin chains also are known. See for example U.S. patent 4,444,878; WO 88/03565; and EP 68,763 and references cited therein.

Ordinarily, the domains of adhesions that are homologous to immunoglobulins and extracellular in their native environment are

5 fused C-terminally to the N-terminus of the constant region of immunoglobulins in place of the variable region(s) thereof, retaining at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain. This
sequence and expressing it in recombinant cell culture. Immunoglobulins and other polypeptides having enhanced plasma half life are fused to the extracellular or ligand binding domains of other adhesons in the same fashion.

10 The boundary domains for the CD4 V-like regions (V1-V4) are, respectively, about 100-109, about 175-184, about 289-298, and about 360-369 (based on the precursor CD4 amino acid sequence in which the initiating met is -25; Fig. 1a). CD4 sequences
15 containing any of the CD4 V domains are fused to the immunoglobulin sequence. It is preferable that the V1V2 or V1V2V3V4 be fused at their C-termini to the immunoglobulin constant region. The precise site at which the fusion is made is not critical; the boundary domains noted herein are for guidance only and other sites
20 neighboring or within the V regions may be selected in order to optimize the secretion or binding characteristics of the CD4. The optimal site will be determined by routine experimentation. In general, it has been found that the fusions are expressed intracellularly, but a great deal of variation is encountered in
25 the degree of secretion of the fusions from recombinant hosts. For instance, the following table demonstrates the various immunoglobulin fusions that have been obtained by the method of this invention. In all examples of CD4 immunoadhesons, the CD4 signal was used to direct secretion from 293 cells. Lower case m represents murine origin, while the lower case h designates human origin. V and C are abbreviations for immunoglobulin variable and constant domains respectively. The numerical subscripts indicate the number of parenthetical units found in the designated multimer. It will be understood that the chains of the multimers are believed
30 to be disulfide bonded in the same fashion as native

-11-

immunoglobulins. The CD4 immunoadhesons typically contained either the first N-terminal 366 residues of CD4 (CD4₄) or the first 180 N-terminal residues of CD4 (CD4₂) linked at their C-terminus to the κ (light) chain or IgG1 heavy chain constant region (γ 1).

5

Table I

Transfected Gene	Secreted Product
$mV_{\kappa}C_{\kappa}$	$mV_{\kappa}C_{\kappa}$ and/or $(mV_{\kappa}C_{\kappa})_2$
10 $mV_{\gamma}1C_{\gamma}1$	ND
$mV_{\kappa}C_{\kappa} + mV_{\gamma}1C_{\gamma}1$	$(mV_{\kappa}C_{\kappa})_2(mV_{\gamma}1C_{\gamma}1)_2 +$ $mV_{\kappa}C_{\kappa}$ and/or $(mV_{\kappa}C_{\kappa})_2$
15 $hCD4-mC_{\kappa}$	$hCD4-mC_{\kappa}$ and/or $(hCD4-mC_{\kappa})_2$
$hCD4-mC_{\gamma}1$	ND
$hCD4-mC_{\kappa} + hCD4-mC_{\gamma}1$	$(hCD4-mC_{\kappa})_2(hCD4-mC_{\gamma}1)_2 +$ $hCD4-mC_{\kappa}$ and/or $(hCD4-mC_{\kappa})_2$
20 $hCD4-hC_{\kappa}$	$hCD4-hC_{\kappa}$ and/or $(hCD4-hC_{\kappa})_2$
$hCD4-hC_{\gamma}1$	$(hCD4-hC_{\gamma}1)_2$
25 $hCD4-hC_{\kappa} + hCD4-hC_{\gamma}1$	$(hCD4-hC_{\kappa})_2(hCD4-hC_{\gamma}1)_2 +$ $hCD4-hC_{\kappa}$ and/or $(hCD4-hC_{\kappa})_2$
$mV_{\kappa}C_{\kappa} + hCD4-hC_{\gamma}1$	$(mV_{\kappa}C_{\kappa})_2(hCD4-hC_{\gamma}1)_2 +$ $mV_{\kappa}C_{\kappa}$ and/or $(mV_{\kappa}C_{\kappa})_2$
30	

*ND = Not detected

35 It is interesting to observe from this table that the CD4-human heavy chain immunoadheson was secreted as a dimer whereas the analogous murine construction was not detected (this not excluding

-12-

the intracellular accumulation of the protein, however). The ability of the hCD4-hCγ1 transformants to produce heavy chain dimer was unexpected since previous work had suggested that immunoglobulin heavy chains are not secreted unless the hosts are cotransformed with nucleic acid encoding both heavy and light chain (Valle et al., *Nature* 241:338 [1981]). According to this invention, CD4-IgG immunoadheson chimeras are readily secreted wherein the CD4 epitope is present in heavy chain dimers, light chain monomers or dimers, and heavy and light chain heterotetramers wherein the CD4 epitope is present fused to one or more light or heavy chains, including heterotetramers wherein up to and including all four variable region analogues are derived from CD4. Where light-heavy chain non-CD4 variable domain is present, a heterofunctional antibody thus is provided.

Various exemplary hetero-and chimeric immunoadheson antibodies produced in accordance with this invention are schematically diagrammed below. "A" means at least a portion of the extracellular domain of an adhesion containing its ligand binding site; V_L, V_H, C_L and C_H represent light or heavy chain variable or constant domains of an immunoglobulin; n is an integer; and Y designates a covalent cross-linking moiety.

- (a) A_{C_L};
- (b) A_{C_L}-A_{C_L};
- (c) A_{C_H}-[A_{C_H}, A_{C_L}-A_{C_H}, A_{C_L}-V_HC_H, V_LC_L-A_{C_H}, or V_LC_L-V_HC_H];
- (d) A_{C_L}-A_{C_H}-[A_{C_H}, A_{C_L}-A_{C_H}, A_{C_L}-V_HC_H, V_LC_L-A_{C_H}, or V_LC_L-V_HC_H];
- (e) A_{C_L}-V_HC_H-[A_{C_H}, A_{C_L}-A_{C_H}, A_{C_L}-V_HC_H, V_LC_L-A_{C_H}, or V_LC_L-V_HC_H];
- (f) V_LC_L-A_{C_H}-[A_{C_H}, A_{C_L}-A_{C_H}, A_{C_L}-V_HC_H, V_LC_L-A_{C_H}, or V_LC_L-V_HC_H];
- or
- (g) [A-Y]_n-[V_LC_L-V_HC_H]₂.

The structures shown in this table show only key features, e. g. they do not show joining (J) or other domains of the immunoglobulins, nor are disulfide bonds shown. These are omitted in the interests of brevity. However, where such domains are

-13-

required for binding activity they shall be construed as being present in the ordinary locations which they occupy in the adhesion, immunoadhesion or immunoglobulin molecules as the case may be. These examples are representative of divalent antibodies; more complex structures would result by employing immunoglobulin heavy chain sequences from other classes, e.g. IgM. The immunoglobulin V_LV_H antibody combining site also designated as the companion immunoglobulin, preferably is capable of binding to a predetermined antigen.

Suitable companion immunoglobulin combining sites and fusion partners are obtained from IgG-1, -2, -3, or -4 subtypes, IgA, IgE, IgD or IgM, but preferably IgG-1.

A preferred embodiment is a fusion of an N-terminal portion of CD4, which contains the binding site for the gp120 envelope protein of HIV, to the C-terminal F_c portion of an antibody, containing the effector functions of immunoglobulin G₁. There are two preferred embodiments of this sort; in one, the entire heavy chain constant region is fused to a portion of CD4; in another, a sequence beginning in the hinge region just upstream of the papain cleavage site which defines IgG F_c chemically (residue 216, taking the first residue of heavy chain constant region to be 114 [Kabat et al., "Sequences of Proteins of Immunological Interest" 4th Ed., 1987]), or analogous sites of other immunoglobulins) is fused to a portion of CD4. These embodiments are described in the examples.

More particularly, those variants in which one or more immunoglobulin-like domains of an adhesion are substituted for the variable region of an immunoglobulin chain are believed to exhibit improved in vivo plasma half life. These chimeras are constructed in a fashion similar to chimeric antibodies in which a variable domain from an antibody of one species is substituted for the variable domain of another species. See, for example, EP 0 125 023; Munro, Nature 312: (13 December 1984); Neuberger et al.,

-14-

Nature 312: (13 December 1984); Sharon et al., Nature 309: (24 May 1984); Morrison et al., Proc. Natl. Acad. Sci. USA 81:6851-6855 (1984); Morrison et al. Science 229:1202-1207 (1985); and Boulianne et al., Nature 312:643-646 (13 December 1984). The DNA encoding the adhesion immunoglobulin-like domain(s) is cleaved by a restriction enzyme at or proximal to the 3' end of the DNA encoding the immunoglobulin-like domain(s) and at a point at or near the DNA encoding the N-terminal end of the mature adhesion polypeptide (where use of a different leader is contemplated) or at or proximal to the N-terminal coding region for the adhesion (where the native adhesion signal is employed). This DNA fragment then is readily inserted into DNA encoding an immunoglobulin light or heavy chain constant region and, if necessary, tailored by deletional mutagenesis. Preferably, this is a human immunoglobulin when the variant is intended for in vivo therapy for humans. DNA encoding immunoglobulin light or heavy chain constant regions is known or readily available from cDNA libraries or is synthesized. See for example, Adams et al., Biochemistry 19:2711-2719 (1980); Gough et al., Biochemistry 19:2702-2710 (1980); Dolby et al., P.N.A.S. USA, 77:6027-6031 (1980); Rice et al., P.N.A.S. USA 79:7862-7865 (1982); Falkner et al., Nature 298:286-288 (1982); and Morrison et al., Ann. Rev. Immunol. 2:239-256 (1984).

DNA encoding the immunoglobulin or immunoadhesion chimeric chain(s) is transfected into a host cell for expression. If the host cell is producing an immunoglobulin prior to transfection then one need only transfect with the adhesion fused to light or to heavy chain to produce a heteroantibody. The aforementioned immunoglobulins having one or more arms bearing the adhesion domain and one or more arms bearing companion variable regions result in dual specificity for adhesion ligand and for an antigen. These are produced by the above-described recombinant methods or by in vitro procedures. In the latter case, for example, F(ab')₂ fragments of the adhesion fusion and an immunoglobulin are prepared, the F(ab')₂ fragments converted to Fab' fragments by reduction under mild

-15-

reducing conditions, and then reoxidized in each other's presence under acidic conditions in accord with methods known *per se*. See also U.S. patent 4,444,878.

5 Additionally, procedures are known for producing intact heteroantibodies from immunoglobulins having different specificities. These procedures are adopted for the *in vitro* production of heterochimeric antibodies by simply substituting the immunoadhesion chains for one of the previously employed
10 immunoglobulins.

In an alternative method for producing a heterofunctional antibody, host cells producing an adhesion-immunoglobulin fusion, e.g. transfected myelomas, also are fused with B cells or
15 hybridomas which secrete antibody having the desired companion specificity for an antigen. Heterobifunctional antibody is recovered from the culture medium of such hybridomas, and thus may be produced somewhat more conveniently than by conventional *in vitro* resorting methods (EP 68,763).

20 Another group of fusions are those in which an adhesion is conjugated with a toxic substance, e.g. a polypeptide such as ricin (including deglycosylated ricin A chain), diphtheria toxin A, or a non-peptidyl cytotoxin. Where the toxin is a polypeptide it is
25 convenient to cross-link the polypeptide to the adhesion or its transmembrane-deleted variant by conventional *in vitro* protein cross-linking agents (for suitable methods for linking ricin A chain or deglycosylated A chain to CD4 see, for example, Duncan et al., "Analy. Biochem." 132:68-73 [1983]; Thorpe et al., "Cancer Res." 47:5924 [1987]; and Ghotie et al., "Cancer Res." 48:2610
30 [1988]) or by recombinant synthesis as a fusion (see for example, U.S. Patent 4,765,382). Alternatively, where companion antibodies are anti-ricin antibody immunoglobulin variable domains, such immunoglobulin heteroantibodies are employed to deliver ricin to

-16-

HIV infected cells following the general procedure of Raso et al.,
Cancer Research, 41:2073 (1981).

Another class of adhesion variants are deletional variants.
5 Deletions are characterized by the removal of one or more amino
acid residues from a adhesion sequence. Typically, the
transmembrane and cytoplasmic domains of adhesions are deleted. In
the case of CD4, at least residues 368 to 395 (the transmembrane
region), and ordinarily 396-433 as well (the cytoplasmic domain),
10 will be deleted to obtain secreted forms of this adhesion.
Parenthetically, the amino acid residues follow the numbers given
for mature CD4 as noted, for example, in figures 1a - 1c. Thus,
CD4T molecules generally will terminate in the vicinity of about
residues 366-368, or at any other suitable site N-terminal thereto
15 which preserves the gp120-binding capability of the CD4 variant.

Substitutional variants are those in which at least one
residue in the adhesion sequence has been removed and a different
residue inserted in its place. The native N-terminal residue for
20 mature CD4 is now known to be lysine. Thus, the sequence shown in
Fig. 1, with an N-terminal asparagine, is an amino acid sequence
variant of native mature CD4. Table 2 below describes
substitutions which in general will result in fine modulation of
the characteristics of the CD antigen.

25

TABLE 2

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>
	Ala	ser
	Arg	lys
5	Asn	gln; his
	Asp	glu
	Cys	ser; ala
	Gln	asn
	Glu	asp
10	Gly	pro
	His	asn; gln
	Ile	leu; val
	Leu	ile; val
	Lys	arg; gln; glu
15	Met	leu; ile
	Phe	met; leu; tyr
	Ser	thr
	Thr	ser
	Trp	tyr
20	Tyr	trp; phe
	Val	ile; leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in adhesion properties will be those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteinyl or prolyl is substituted for (or by) any other residue; (c) a residue having

-18-

an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanyl, is substituted for (or by) one not having a side chain, e.g., glycyl.

A preferred class of substitutional or deletional variants are those involving the transmembrane region of the adhesion. The transmembrane region of the adhesion is a highly hydrophobic or lipophilic domain that is the proper size to span the lipid bilayer of the cellular membrane. It is believed to anchor the adhesion in the cell membrane.

Deletion or substitution of the transmembrane domain will facilitate recovery and provide a soluble form of the adhesion by reducing its cellular or membrane lipid affinity and improving its water solubility. If the transmembrane and cytoplasmic domains are deleted one avoids the introduction of potentially immunogenic epitopes, either by exposure of otherwise intracellular polypeptides that might be recognized by the body as foreign or by insertion of heterologous polypeptides that are potentially immunogenic. A principal advantage of the transmembrane deleted adhesion is that it is secreted into the culture medium of recombinant hosts. This variant is water soluble and does not have an appreciable affinity for cell membrane lipids, thus considerably simplifying its recovery from recombinant cell culture.

It will be amply apparent from the foregoing discussion that substitutions, deletions, insertions or any combination thereof are introduced to arrive at a final construct. As a general proposition, all variants will not have a functional transmembrane domain and preferably will not have a functional cytoplasmic sequence. This is generally accomplished by deletion of the relevant domain, although adequate insertional or substitutional mutagens also can be effective for this purpose.

-19-

For example, the transmembrane domain is substituted by any amino acid sequence, e.g. a random or homopolynucleic sequence of about 5 to 50 serine, threonine, lysine, arginine, glutamine, aspartic acid and like hydrophilic residues, which altogether exhibit a hydrophilic hydropathy profile, so that it is secreted into the culture medium of recombinant hosts. This variant should also be considered to be an adhesion variant.

These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the adhesion, thereby producing DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture. However, variant adhesions also are prepared by *in vitro* synthesis. Obviously, variations made in the DNA encoding the variant adhesions must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure deleterious to expression (EP 75,444A). The CD4 variants typically exhibit the same gp120 binding activity as does the naturally-occurring prototype, although variants also are selected in order to modify the characteristics of the CD4 adhesion as indicated above.

While the site for introducing an amino acid sequence variation is predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed adhesion variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example M13 primer mutagenesis.

Adhesion variants that are not capable of binding HIV gp120 are useful nonetheless as immunogens for raising antibodies to the adhesion or as immunoassay kit components (labelled, as a competitive reagent for gp120 assay, or unlabelled as a standard.

-20-

for an adhesion assay) so long as at least one adhesion epitope remains active.

The DNA encoding adhesions is obtained by known procedures. See Williams, Immunol. Today 8:298-303 (1987) and citations therein. In general, prokaryotes are used for cloning of CD4 variant DNA sequences. For example, *E. coli* strain SR101 (for propagating m13 phage, a λ -resistant strain of JM 101; Messing et al., Nucl. Acids. Res. 2(2):309-321 [1981]); and *E. coli* K12 strain 294 (ATCC No. 31446) are particularly useful. Other microbial strains which may be used include *E. coli* B, UM101 and *E. coli* x1776 (ATCC No. 31537). These examples are illustrative rather than limiting.

DNA encoding the variant adhesions are inserted for expression into vectors containing promoters and control sequences which are derived from species compatible with the intended host cell. The vector ordinarily, but need not, carry a replication site as well as one or more marker sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using a derivative of pBR322 which is a plasmid derived from an *E. coli* species (Bolivar, et al., Gene 2: 95 [1977]). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid must also contain or be modified to contain promoters and other control elements commonly used in recombinant DNA constructions.

Promoters suitable for use with prokaryotic hosts illustratively include the β -lactamase and lactose promoter systems (Chang et al., Nature, 275: 615 [1978]; and Goeddel et al., Nature 281: 544 [1979]), alkaline phosphatase, the tryptophan (*trp*) promoter system (Goeddel, Nucleic Acids Res. 8: 4057 [1980] and EPO Appln. Publ. No. 36,776) and hybrid promoters such as the *tac*

-21-

promoter (H. de Boer et al., Proc. Natl. Acad. Sci. USA 80: 21-25 [1983]). However, other functional bacterial promoters are suitable. Their nucleotide sequences are generally known, thereby enabling a skilled worker operably to ligate them to DNA encoding the adhesion variant using linkers or adaptors to supply any required restriction sites (Siebenlist et al., Cell 20: 269 [1980]). Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the antigen.

In addition to prokaryotes, eukaryotic microbes such as yeast cultures also are useful as cloning or expression hosts. Saccharomyces cerevisiae, or common baker's yeast is the most commonly used eukaryotic microorganism, although a number of other strains are commonly available. For expression in Saccharomyces, the plasmid YRp7, for example, (Stinchcomb, et al., Nature 282: 39 [1979]; Kingsman et al. Gene 2: 141 [1979]; Tschemper et al., Gene 10: 157 [1980]) is commonly used. This plasmid already contains the trp1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example ATCC no. 44076 or PEP4-1 (Jones, Genetics 85: 12 [1977]). The presence of the trp1 lesion as a characteristic of the yeast host cell genome then provides an effective means of selection by growth in the absence of tryptophan.

Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., J. Biol. Chem. 255: 2073 [1980]) or other glycolytic enzymes (Hess et al., J. Adv. Enzyme Reg. 2: 149 [1968]; and Holland, Biochemistry 17: 4900 [1978]), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

-22-

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman et al., European Patent Publication No. 73,657A. Yeast enhancers also are advantageously used with yeast promoters.

Promoters for controlling transcription from vectors in mammalian host cells may be obtained from various sources, for example, the genomes of viruses such as: polyoma, Simian Virus 40 (SV40), adenovirus, retroviruses, hepatitis-B virus and most preferably cytomegalovirus, or from heterologous mammalian promoters, e.g. the beta actin promoter. The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment which also contains the SV40 viral origin of replication. Fiers et al., Nature, 273: 113 (1978). The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. Greenaway, P.J. et al., Gene 18: 355-360 (1982). Of course, promoters from the host cell or related species also are useful herein.

DNA transcription in higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually from about 10 to 300bp, that act to increase the transcription initiation capability of a promoter. Enhancers are relatively orientation and position independent having been found 5' (Laimins, L. et al., Proc.Natl.Acad.Sci. 78: 993 [1981]) and 3' (Lusky, M.L., et al., Mol. Cell Bio. 3: 1108 [1983]) to the transcription unit, within an intron (Banerji, J.L. et al., Cell 33: 729 [1983]) as well as within the coding sequence itself (Osborne, T.F., et al., Mol. Cell Bio. 4: 1293 [1984]).

-23-

Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human or nucleated cells) may also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA encoding the adhesion.

Expression vector systems generally will contain a selection gene, also termed a selectable marker. Examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR), thymidine kinase or neomycin. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective pressure. There are two widely used distinct categories of selective regimes. The first category is based on a cell's metabolism and the use of a mutant cell line which lacks the ability to grow independent of a supplemented medium. Two examples are: CHO DHFR⁻ cells and mouse LTK⁻ cells. These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented medium. An alternative to supplementing the medium is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells which were not transformed with the

-24-

DHFR or TK gene will not be capable of survival in non supplemented media.

5 The second category is dominant selection which refers to a selection scheme used in any cell type and does not require the use of a mutant cell line. These schemes typically use a drug to arrest growth of a host cell. Those cells which have a novel gene would express a protein conveying drug resistance and would survive the selection. Examples of such dominant selection use the drugs
10 neomycin, Southern P. and Berg, P., J. Molec. Appl. Genet. 1: 327 (1982), mycophenolic acid, Mulligan, R.C. and Berg, P. Science 209: 1422 (1980) or hygromycin, Sugden, B. et al., Mol. Cell. Biol. 5: 410-413 (1985). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the
15 appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid) or hygromycin, respectively.

"Amplification" refers to the increase or replication of an isolated region within a cell's chromosomal DNA. Amplification
20 is achieved using a selection agent e.g. methotrexate (MTX) which inactivates DHFR. Amplification or the making of successive copies of the DHFR gene results in greater amounts of DHFR being produced in the face of greater amounts of MTX. Amplification pressure is applied notwithstanding the presence of endogenous DHFR, by adding
25 ever greater amounts of MTX to the media. Amplification of a desired gene can be achieved by cotransfecting a mammalian host cell with a plasmid having a DNA encoding a desired protein and the DHFR or amplification gene permitting coinfection. One ensures that the cell requires more DHFR, which requirement is met by
30 replication of the selection gene, by selecting only for cells that can grow in the presence of ever-greater MTX concentration. So long as the gene encoding a desired heterologous protein has coinfection with the selection gene replication of this gene gives rise to replication of the gene encoding the desired protein. The
35 result is that increased copies of the gene, i.e. an amplified

-25-

gene, encoding the desired heterologous protein express more of the desired heterologous protein.

Preferred host cells for expressing the CD antigen variants of this invention are mammalian cell lines, examples including: monkey kidney CV1 line transformed by SV40 (COS-7; ATCC CRL 1651); human embryonic kidney line (293; Graham, F.L. et al.; J. Gen Virol. 36: 59 [1977] and 293S cells [293 subclones selected for better suspension growth]); baby hamster kidney cells (BHK; ATCC CCL 10); chinese hamster ovary-cells-BHK (CHO; Urlaub and Chasin, Proc Natl Acad Sci. (USA) 77: 4216, [1980]); mouse sarco1 cells (TM4; Mather, J.P., Biol. Reprod. 23: 243-251 [1980]); monkey kidney cells (CV1 ATCC CCL 70); african green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA; ATCC CCL 2); canine kidney cells (MDCK; ATCC CCL 34); buffalo rat liver cells (BRL 3A; ATCC CRL 1442); human lung cells (W138; ATCC CCL 75); human liver cells (Hep G2; HB 8065); mouse mammary tumor (MST 069362, ATCC CCL51 cells); and TRI cells (Mather, J.P. et al., Annals N.Y. Acad. Sci. 383: 44-68 [1982]).

"Transformation" means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integration. One suitable for transformation of the host cells is the method of Graham, F. and van der Eb, A., Virology 52: 456-457 (1973). However, other methods for introducing DNA into cells such as by nuclear injection or by protoplast fusion may also be used. If prokaryotic cells or cells which contain substantial cell walls are used as hosts, the preferred method of transfection is calcium treatment using calcium chloride as described by Cohen, F.N. et al., Proc. Natl. Acad. Sci. (USA), 62: 2110 (1972).

Construction of suitable vectors containing the desired coding and control sequences employ standard and manipulative ligation techniques. Isolated plasmids or DNA fragments are

-26-

cleaved, tailored, and religated in the form desired to form the plasmids required. Suitable procedures are well known for the construction described herein. See, for example, (Maniatis, T. et al., Molecular Cloning, 133-134 Cold Spring Harbor, [1982];
5 "Current Protocols in Molecular Biology", edited by Ausubel et al., [1987], pub. by Greene Publishing Associates & Wiley-Interscience).

Correct plasmid sequences are confirmed by transforming *E. coli* K12 strain 294 (ATCC 31446) with ligation mixtures, successful
10 transformants selected by ampicillin or tetracycline resistance where appropriate, plasmids from the transformants prepared, and then analyzed by restriction enzyme digestion and/or sequenced by the method of Messing et al., *Nucleic Acids Res.* 2: 309 (1981) or by the method of Maxam et al., *Methods in Enzymology* 65: 499
15 (1980).

Host cells are transformed with the expression vectors of this invention. Thereafter they are cultured in appropriate culture media, e.g. containing substances for inducing promoters,
20 selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

25 The secreted adhesion variants are recovered and purified from the culture supernatants or lysates of recombinant hosts. Typically, the supernatants are concentrated by ultrafiltration, contacted with a ligand affinity or immunoaffinity matrix so as to adsorb the adhesion variant, and eluted from the matrix.
30 Optionally, the adhesion is purified by ion exchange chromatography.

Surprisingly, purification of soluble CD4 adhesion from culture medium was unexpectedly difficult. Notwithstanding that the hydrophobic transmembrane region of the antigen had been
35 deleted, the antigen exhibited a strong tendency to form aggregates

-27-

that could be readily removed from suspension by centrifugation at 1000 x g, and which avidly coat surfaces such as ultrafiltration membranes. This appears to result from the reduction in concentration of albumin or other serum protein (ordinarily present in the crude preparation) to a particular level, below which the truncated antigen no longer remains soluble. This phenomenon appears to be aggravated by exposure of the CD4 adhesion to low pH (< about pH 4). As a result, separation procedures (particularly those that employ acid elution, such as immunoaffinity) should be modified so that the eluate is maintained at, or immediately returned to, about neutrality. Further, a surfactant, e.g. a detergent such as Tween 80, should be included with the antigen during the separation procedure. The final purified product will be stabilized with a predetermined protein such as albumin, and/or a detergent.

The purified adhesion is formulated into conventional pharmacologically acceptable excipients.

It is administered to patients having HIV infection at a dosage capable of maintaining a concentration of greater than about 100 ng of soluble CD4 adhesion/ml plasma. For CD4 adhesion variants having different molecular weights, about 2 picomoles of soluble receptor per ml of plasma will be initially evaluated clinically in order to establish a stoichiometric equivalence with native (membrane bound) and soluble receptor. The ordinary dosage of soluble CD4 is 100 µg/kg of patient weight/day.

The therapeutic CD4 variants are employed with other therapies and agents for the treatment of AIDS, including AZT, neutralizing antibodies and immunocytotoxins, gp120 fragments and vaccines.

-28-

In order to facilitate understanding of the following examples certain frequently occurring methods and/or terms will be described.

5 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent
10 plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in
15 the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μ g of plasmid or DNA fragment is used with about 2 units of enzyme in
20 about 20 μ l of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μ g of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation
25 times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

30 "Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the digest on polyacrylamide or agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section
35 containing the desired fragment, and separation of the gel from

-29-

DNA. This procedure is known generally (Lawn, R. et al., *Nucleic Acids Res.* 9: 6103-6114 [1981], and Goeddel, D. et al., *Nucleic Acids Res.* 8: 4057 [1980]).

5 "Dephosphorylation" refers to the removal of the terminal 5' phosphates by treatment with bacterial alkaline phosphatase (BAP). This procedure prevents the two restriction cleaved ends of a DNA fragment from "circularizing" or forming a closed loop that would impede insertion of another DNA fragment at the restriction
10 site. Procedures and reagents for dephosphorylation and other recombinant manipulations are conventional. Reactions using BAP are carried out in 50mM Tris at 68°C to suppress the activity of any exonucleases which may be present in the enzyme preparations. Reactions were run for 1 hour. Following the reaction the DNA
15 fragment is gel purified.

"Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T. et al., *Id.* at 146). Unless otherwise provided, ligation may be
20 accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

"Filling" or "blunting" refers to the procedures by which
25 the single stranded end in the cohesive terminus of a restriction enzyme-cleaved nucleic acid is converted to a double strand. This eliminates the cohesive terminus and forms a blunt end. This process is a versatile tool for converting a restriction cut end that may be cohesive with the ends created by only one or a few
30 other restriction enzymes into a terminus compatible with any blunt-cutting restriction endonuclease or other filled cohesive terminus. Typically, blunting is accomplished by incubating 2-15µg of the target DNA in 10mM MgCl₂, 1mM dithiothreitol, 50mM NaCl, 10mM Tris (pH 7.5) buffer at about 37°C in the presence of 8
35 units of the Klenow fragment of DNA polymerase I and 250 µM of each

-30-

of the four deoxynucleoside triphosphates. The incubation generally is terminated after 30 min. phenol and chloroform extraction and ethanol precipitation.

5 The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention.

Example 1

10 Construction of Vectors for the Expression of Native CD4 and Secreted Derivatives

Section 1

The plasmid used for recombinant synthesis of human CD4 was pSVeCD4DHFR. The plasmid was constructed as follows:

15 λ CD4P1 containing most of the coding sequence of human CD4 (obtained from a human placental cDNA library using oligonucleotide probes based on the published sequence [Maddon et al. 1985]) was digested with EcoRI to produce the cDNA insert. This fragment was recovered by polyacrylamide gel electrophoresis (fragment 1).

20 pUC18 was digested with EcoRI and the single fragment recovered by polyacrylamide gel electrophoresis (fragment 2). Fragment 1 was ligated to fragment 2 and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct DNA fragments. This plasmid is referred to as pUCCD4.

30 pSVeE'DHFR (Muesing et al., Cell 48:691-701 [1987]) was digested with KpnI and BamHI and blunted with *E. coli* DNA polymerase I (Klenow fragment) and the four dNTPs. Fragment 3 containing the pML-Amp^r region, SV40 early promoter, the HIV LTR, and the mouse DHFR gene was recovered by gel electrophoresis.

35

-31-

ligated and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the BamHI restriction site and the absence of the KpnI restriction site. This plasmid is referred to as pSV Δ BKDHFR and allows EcoRI-BamHI fragments to be inserted after the SV40 early promoter and transcribed under its control, following transfection into an appropriate cell line.

Synthetic oligonucleotides (adaptors 1-8, below) were made to extend from 76 bp 5' of the initiation codon of CD4 translation to the RsaI restriction site at 121 bp 3' of the initiator, with the sequence AATT at the 5' end of the sense strand to generate an end which could ligate to an EcoRI restriction fragment. These oligonucleotides were ligated and the 204 bp fragment containing the entire sequence recovered by gel electrophoresis (fragment 4).

CD4 adaptor 1: AATTCAAGCCCAGAGCCCTGCCATTCTGTGGGCTCAGGTCCCT
CD4 adaptor 2: PACTGCTCAGCCCTTCCTCCCTCGGCAAGGCCACAATGAACCGGGAGTC
CD4 adaptor 3: PCCTTTTAGGCACTTGCTTCTGCTGCTGCAACTGGCGCTCCTCCAGC
CD4 adaptor 4:
PAGGCACTCAGGGAACAAAGTGGTGCTGGGCAAAAAGGGGATACAGTGGAAGTACCTGT
CD4 adaptor 5: PACAGGTCAGTTCAGTGTATCCCCTTTTGGCCAGCACCAGTTTGTTC
CD4 adaptor 6: PCTGAGTGGCTGCTGGGAGGAGCGCCAGTTGCAGCACCAGAAGCAAGT
CD4 adaptor 7: PGCCATAAAGGGACTCCCGGTTTCATTGTGGCCTTGCCGAGGGAGGAAGGC
CD4 adaptor 8: GCTGAGCACTAGGGACCTGAGCCACAGAAATGGCAGGGCTCTGGGCTTG

pUCCD4 was digested with RsaI and SstI and the 401 bp fragment containing part of the CD4 coding sequence recovered by gel electrophoresis (fragment 5). pUC18 was digested with EcoRI and SstI and the fragment comprising the bulk of the plasmid recovered by gel electrophoresis (fragment 6). Fragments 4 and 5 were ligated to fragment 6 and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on

-32-

ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The sequence of the inserted synthetic DNA was checked by excising the 605 bp EcoRI-SstI fragments from several transformants and ligating them to M13mp19 which had been digested with the same enzymes. After transformation into *E. coli* strain JM101, single-stranded DNA was prepared and sequenced. One plasmid which contained the correct sequence was selected, and is referred to as pCD4int.

pCD4int was digested with EcoRI and SstI and fragment 7 containing the 5' end of the CD4 coding region was recovered by gel electrophoresis. pUCCD4 was digested with SstI and BamHI and the 1139 bp fragment containing the remainder of the CD4 coding region (fragment 8) recovered by gel electrophoresis.

pSV Δ BKDHFR was digested with EcoRI and BamHI and fragment 9 comprising the bulk of the plasmid was isolated. Fragments 7, 8 and 9 were ligated and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and the resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. This plasmid is referred to as pSV Δ CD4DHFR, and was used to direct synthesis of recombinant intact CD4.

Section 2

A plasmid was constructed to direct the synthesis of a CD4 derivative lacking the putative transmembrane domain and most of the putative cytoplasmic domain (Maddon et al.). This was done with the intention of creating a secreted form of CD4, based on the assumption that these domains anchor the CD4 glycoprotein to the cell membrane, and that their deletion would result in the secretion of the product. This plasmid is referred to as pSV Δ CD4 Δ N1 Δ DHFR and was constructed as follows:

-33-

pUCCD4 was digested with SstI and TaqI and the 531 bp fragment (fragment 10) recovered. pUCCD4 was digested with NlaIII and TaqI and the 112 bp fragment (fragment 11) recovered. pUCCD4 was digested with BamHI and NlaIII and the 301 bp fragment (fragment 12) recovered. pCD4int was digested with SstI and BamHI and fragment 13 comprising the bulk of the plasmid recovered. Fragments 10, 11, and 12 were ligated together with fragment 13 and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. Plasmid DNA from several transformants was sequenced to ensure that the 195 bp NlaIII fragment had been deleted and that the proper reading frame was restored. The resulting plasmid is referred to as pCD4ΔNla.

pCD4ΔNla was digested with EcoRI and BamHI and the 1541 bp fragment containing the sequence of a CD4 derivative lacking the transmembrane and cytoplasmic domains recovered (fragment 14) and ligated to fragment 9 and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. This plasmid is referred to as pSVeCD4ΔNlaDHFR.

Both pSVeCD4DHFR and pSVeCL4ΔNlaDHFR were transfected into CHO cells by the same method used to establish cell lines stably expressing HIV-1 polypeptides (Muesing, Smith and Capon, Cell 48:6910701 [1987]). These cells were assayed for production by radioimmunoprecipitation as described below. While no product was detected in initial experiments, subsequent experiments showed that the above described coding segment could indeed direct the

-34-

synthesis of a soluble CD4 adhesion variant both in CHO and 293 cells.

Section 3

5 A different expression system was initially used for the synthesis and expression of a CD4 variant lacking completely the cytoplasmic and transmembrane domains. This system uses the cytomegalovirus promoter and can be used in cultured cells of human origin. The first plasmid constructed for use in this system
10 contained the entire coding region for CD4 and was intended to function as a control in the following studies. It is referred to as pRKCD4, and was constructed as follows:

pSVeCD4DHFR was digested with EcoRI and BamHI and fragment
15 containing the entire CD4 coding region was isolated. pRK5 (U.S.S.N. 97,472, filed Sept. 11, 1987) was digested with EcoRI and BamHI and fragment 16 comprising the bulk of the plasmid recovered by gel electrophoresis, ligated to fragment 15, and the ligation mixture transformed into *E. coli* strain 294. The transformed
20 culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. This plasmid is referred to as pRKCD4.

Section 4

The next plasmid constructed was designed to direct the expression of the above-mentioned (Section 3) secreted derivative of CD4. The coding region of CD4 was fused after amino acid
30 residue 368 of mature CD4 to a sequence from pBR322 which codes for 9 more residues before a translation termination codon. This removes the putative CD4 transmembrane and cytoplasmic domains, which are presumed to anchor CD4 to the cell surface. The plasmid is referred to as pRKCD4T (and which produces protein called CD4T), and was constructed as follows:

35

-35-

pSVeCD4DHFR was digested with HpaII, blunted with Klenow fragment and the four dNTPs, and digested with BstEII. The 382 bp fragment (fragment 17) containing part of the CD4 coding sequence was recovered by gel electrophoresis. pSVeCD4DHFR was digested with EcoRI and BstEII and the 874 bp fragment (fragment 18) recovered. pBR322 was digested with HindIII, blunted with Klenow fragment and the four dNTPs, and digested with EcoRI. Fragment 19 comprising the bulk of the plasmid was isolated and ligated to fragments 17 and 18 and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. This plasmid is referred to as pCD4Tint.

pRK5 was digested with EcoRI and SmaI and fragment 20 comprising the bulk of the plasmid isolated. pCD4Tint was digested with EcoRI and EcoRV and the 1410 bp fragment containing the CD4 coding sequence to the HpaII site at 1176 bp 3' of the initiating codon and the 154 bp HindIII-EcoRV fragment of pBR322 was recovered (fragment 21). Fragments 20 and 21 were ligated and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. This plasmid is referred to as pRKCD4T.

Section 5a

In order to create a secreted form of CD4 which could be purified with an antibody directed to herpes virus type I glycoprotein D, a plasmid was constructed to express a derivative of CD4T in which the region coding for the mature, processed CD4T polypeptide was fused to a sequence coding for the signal peptide and the first 27 residues of the mature type I Herpes Simplex Virus

-36-

gD glycoprotein. This plasmid is referred to as pRKGD4T, and was constructed as follows:

5 pgDTrunc.DHFR was digested with EcoRI and PvuII and the fragment containing the coding region for the signal peptide and first 27 residues of the mature HSV I gD glycoprotein was isolated (fragment 22). pRKCD4T was digested with EcoRI and BstEII and fragment 23 containing the 3' end of the CD4 coding sequence and the pRK5 region was isolated.

10

Synthetic oligonucleotides GD (adaptors 1-2, below) containing the coding sequence of CD4 from the codon for the amino terminal residue of mature CD4 to the Rsa site at 121 bp 3' of translation initiation, and containing the sequence CTGCTCGAG at the 5' end of the sense strand were prepared (fragment 24). pRKCD4 was digested with RsaI and BstEII and the 665 bp fragment containing part of the coding region for CD4 was recovered (fragment 25) and ligated to fragment 24. After digestion with BstEII to ensure that only monomeric fragment was present, the 724 bp fragment containing both sequences was recovered by gel electrophoresis (fragment 26).

15

20

Fragments 22, 23 and 26 were ligated and the ligation mixture transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The sequence of several transformants was checked to ensure that the synthetic insert was correct and that reading frame was preserved. This plasmid is referred to as pRKGD4T.

25

30

These pRK5 derived plasmids preferably were transfected into 293S cells for stable expression according to Muesing, et al. Cell 48:691 (1987) with the exception that in addition to the plasmid of interest a plasmid expressing the neomycin resistance

35

-37-

gene pRSV neo (Gorman et al. Science 221:553-555 (1985)) was cotransfected. 293 cells also are used satisfactorily as host cells. 2 days after transfection, the cells were passaged into standard medium (1:1 F12/DME supplemented with L-glutamine, penicillin-streptomycin and 10% FBS) with 0.5 mg/ml G418 (Genticin sulfate; Gibco) for selection of stable cell lines, rather than in media containing methotrexate as shown by Muesing et al. Cells were assayed for production of CD4 or CD4 analogs by radioimmuno-precipitation. Binding studies (section 5c) used conditioned supernatants from these cells in the 1:1 F12/DME medium. Materials used in infectivity assays (section 5b) were obtained as described in section 8 below.

gDCD4 adaptor 1:

CTGCTCGAGCAGCGAAACAAAGTGGTCTGGGCAAAAAGGGGATACACTGGAAGTGC

gDCD4 adaptor 2:

PACAGGTCAGTTCCTGATATCCCTTTTGGCCAGCAGCACTTTGTTTCCCTGCTCGA

Section 5b

The following constitutes a study of the neutralization of HIV-1 infectivity by soluble CD4 analogs. A modification of the neutralization procedure of Robert-Guroff et al., Nature 316:72 (1985) was followed. Equal volumes of inhibitor supernatant and virus (60 microliters) were incubated at 4 degrees C for 1 hour, then the same volume of H9 (Gallo et al., Science 224:500, 1984) at 5×10^6 /ml was added and incubation continued for 1 hour at 37 degrees C. Following absorption, 2.5×10^5 cells in 150 microliters were transferred to 2 ml of incubation media. After 4 days at 37 degrees C, the cultures were split 1:2 with fresh media and incubated for an additional 3 days. Cultures were harvested, reverse transcriptase activity was measured (Groopman et al., AIDS Research and Human Retroviruses 1:71, 1987), and immunofluorescence reactivity with HIV-1 positive serum was determined as described (Polesz et al., Proc. Acad. Nat. Sci. USA 77:7415, 1980).

-38-

Inhibitor supernatants were obtained from confluent plate cultures of 293S/CDT4, 293S/gDCD4T cells or untransfected 293S cells by replacing the growth medium incubation media and harvesting the supernatants 24 hours later. Inhibitor supernatant replaced part or all of the incubation media during the first three days of culture as indicated in the second column of Table 3. Challenge dose of virus was 100 TCID₅₀ (Groopman et al., supra) of HIV-1 strain HTLV-III_B grown in H9 cells assayed in the same system. Incubation media consisted of RPMI 1640 media containing 2mM L-glutamine, 100 units/ml penicillin, 100 micrograms/ml streptomycin, 2 micrograms/ml polybrene and 20% fetal calf serum (M.A. Bioproducts).

Table 3

Inhibitor supernatant	Dilution of Inhibitor supernatant	Indirect immunofluorescence (% positive cells)		Reverse transcriptase (cpm/ml x 10 ²)	
mock-trans- fected	undil.; 1:4	65.3	65.5	21.8	23.9
mock-trans- fected	undil.; 1:4	61.2	61.1	18.5	28.1
CD4T	undil.; 1:4	0.4	18.0	0.11	5.94
CD4T	undil.; 1:4	0.8	16.1	0.15	3.72
gDCD4T	undil.; 1:4	0.4	26.8	0.14	9.92
gDCD4T	undil.; 1:4	1.4	36.1	0.23	11.3

Both forms of soluble CD4 virtually abolished the growth of HIV-1, when incubated with virus-infected cells without prior dilution (Table 2). At a dilution of 1:4 the soluble CD4 preparations were only partially effective in inhibiting virus growth, however the level of fluorescent-positive cells and reverse transcriptase was still significantly lower than cultures receiving mock-transfected cell supernatants (Table 2). Since there was no significant difference in virus growth between diluted and

-39-

undiluted control supernatants, nor did any of the supernatants affect the growth of uninfected H9 cells (data not shown), soluble CD4 proteins present in these supernatants were concluded to be responsible for the neutralization of HIV-1 infection of H9 cells.

5

Section 5c

To determine the affinity constant for interactions between gp120 and CD4 or CD4 variants, saturation binding analysis was carried out with soluble CD4 (supra) and detergent solubilized intact CD4 (Lasky et al. Cell 50:975 [1987]) employing radiiodinated gp120 labeled with lactoperoxidase. Binding reactions consisted of ^{125}I -gp120 (3 ng to 670 ng, 2.9 nCi/ng) incubated for 1 hour at 0 degrees C with cell lysates containing intact CD4 (Laskey et al., op cit.) or cell supernatants containing unlabeled CD4T or gDCD4T prepared as described in section 5a. Reactions (0.2ml) had a final composition of 0.5X McDougal Lysis Buffer (McDLB) (1 x McDLB contains 0.5 % Nonidet NP-40, 0.2% Na deoxycholate, 0.12 M NaCl, 0.02 M Tris-HCl, pH 8.0) and were performed in duplicate, both in the presence or absence of 50 micrograms of unlabeled purified gp120 (74 fold or greater excess). Following incubation, bound gp120 was quantitated by immunoprecipitation and counted in a gamma counter. For immunoprecipitation, binding reaction solutions were preabsorbed with 5 microliters of normal rabbit serum for one hour at 0°C, and cleared with 40 microliters of Pansorbin (10 % w/v, Calbiochem) for 30 minutes at 0 degrees C. Samples were then incubated overnight at 0 degrees C with 2 microliters of normal serum or 5 microliters (0.25 microgram) of OKT4 monoclonal antibody (Ortho) followed by collection of immune complexes with 10 microliters of Pansorbin. Precipitates were washed twice in 1X McDLB and once in water, then eluted by eluting at 100 degrees C for 2 minutes in sample buffer (0.12 M Tris-HCl pH 6.8, 4% SDS, 0.7 M mercaptoethanol, 20% glycerol, and 0.1% bromophenol blue). CD4 molecules were bound saturably by gp120, and yielded a simple mass action binding curve.

-40-

Supernatants from mock-transfected cells gave a level of specifically bound gp120 less than 1% that found for supernatants containing soluble CD4. Scatchard analysis revealed a single class of binding sites on each molecule, with apparent dissociation constants (K_d) of 1.3×10^{-9} M, 0.83×10^{-9} M and 0.72×10^{-9} M for intact CD4, CD4T and gDCD4T, respectively. The values obtained for CD4-gp120 binding in solution are comparable to the affinity previously measured for gp120 binding to CD4 on whole cells ($K_d \sim 4.0 \times 10^{-9}$ M. Lasky, Cell, *supra*).

Section 6

In order to produce secreted derivatives of CD4 which are free of extraneous amino acid residues, two plasmids were constructed for expression in 293 cells. The plasmids contain CD4 genes which have been truncated without the addition of extra residues, and are referred to as pRKCD4 Δ N1a and pRKCD4TP (and which produce proteins called CD4TP and CD4 Δ N1a), and were constructed as follows:

Fragment 14 containing the CD4 gene with the 195 bp NlaIII restriction fragment deleted was ligated to fragment 16, which is pRK5 digested with EcoRI and BamHI. The ligation mixture was transformed into *E. coli* strain 294, the transformed culture plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The resulting plasmid is referred to as pRKCD4 Δ N1a.

Synthetic DNA (5'-CGT GAT AGA AGC TTT GTA GAG 3') was made to attach to the HpaII site at 1176bp and which when so attached would terminate translation after amino acid residue 368 of mature CD4 (fragment 27). The other end of this fragment was designed to ligate to BamHI restriction fragments. pUCCD4 was digested with BstEII and HpaII and the 382bp fragment containing part of the CD4 gene was recovered (fragment 28). Fragments 27 and 28 were ligated

-41-

and then digested with BstEII to reduce dimerized fragments to monomers, and the resulting 401bp fragment was recovered (fragment 29).

5 pRKCD4 was digested with BstEII and BamHI and the fragment comprising the bulk of the plasmid (fragment 30) was isolated and ligated to fragment 29. The ligation mixture was transformed into *E. coli* strain 294, the transformed culture plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was
10 prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The resulting plasmid is referred to as pRKCD4TP. Both plasmids are transfected into 293 cells to generate stable variant CD4-expressing cell lines as described above.

15

Section 7

Two plasmids were constructed to direct the expression of secreted CD4 lacking extraneous amino acid residues in CHO cells. These are referred to as pSVeCD4AN1aSVVDHFR and pSVeCD4TPSVVDHFR (and
20 which encode proteins having the primary sequence of CD4AN1a and CD4TP), and were constructed as follows:

pE348HBV.E400D22 was digested with PvuI and EcoRI and the
25 fragment containing the SV40 early promoter and part of the β -lactamase gene was recovered (fragment 31). pE348HBV.E400D22 was digested with PvuI and BamHI and the large fragment containing the balance of the β -lactamase gene as well as the SV40 early promoter and the DHFR gene was isolated (fragment 32).

30

Fragments 31 and 32 were ligated together with fragment 14 and transformed into *E. coli* strain 294. The transformed culture was plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked
35 by restriction analysis for the presence of the correct fragment.

-42-

The resulting plasmid is referred to as pSVECD4ΔN1aSVDHFR. This plasmid contains the same DNA fragment encoding the soluble CD4 molecule found in the above-mentioned plasmid pSVECD4ΔN1aDHFR (Section 2).

5 PRKCD4TP was digested with EcoRI and BamHI and the fragment containing the truncated CD4 coding region was isolated and ligated to fragments 31 and 32. The ligation mixture was transformed into *E. coli* strain 294, the transformed culture plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The resulting plasmid is referred to as pSVECD4TPSVDHFR. Both of these plasmids are transfected into CHO cells and amplified transfectants selected by methotrexate using conventional procedures.

Example 2

20 Fusions of the V region of the CD4 gene, which is homologous to the variable region of immunoglobulin genes (ref Maddon et al. 1985), to the constant (C) region of human immunoglobulin κ and $\gamma 2$ chains are constructed as follows:

25 Synthetic DNA is made to code for the C region of human κ chain (residues 109-214) based on the sequence published by Morin et al., Proc. Natl. Acad. Sci. 82:7025-7029, with the addition at the 5' end of the coding strand of the sequence GGGG, which allows this fragment to be ligated to the BspMI site at the end of the putative V-like region of CD4. At the 3' end of the coding region, a translational stop codon is added as well as a sequence which allows this end to be ligated to BamHI restriction fragments. The synthetic DNA is made in 8 fragments, 4 for each strand, 70-90 bases long. These are then allowed to anneal and ligated prior to isolation on a polyacrylamide gel (fragment 33).

35

-43-

pRKCD4 is digested with EcoRI and BspMI and the 478bp fragment containing the region coding for the putative V-like domain of CD4 is recovered (fragment 34). Fragments 33 and 34 are ligated together with fragment 16 (from the expression vector pRK5). The ligation mixture is transformed into *E. coli* strain 294, the transformed culture plated on ampicillin media plates and resistant colonies selected. Plasmid DNA is prepared from transformants and checked by restriction analysis for the presence of the correct fragment. The resulting plasmid is referred to as pRKCD4Ck.

A plasmid encoding a fusion of the CD4 V-like domain to the human immunoglobulin C γ 2 region is constructed in a similar fashion, and is referred to as pRKCD4C γ 2. Both of these plasmids are transfected into 293 cells, myeloma cells or other competent cells in order to obtain cell lines expressing variant CD4 molecules as described above.

Example 3

The gDCD4T secreted by the method of Example 1 was purified from cell culture fluid containing either 10% FBS (fetal bovine serum) or no added FBS. The conditioned cell culture fluid was first concentrated by ultrafiltration then purified by immunoaffinity chromatography. The immunoaffinity column was produced by coupling murine monoclonal antibody 5B6 (whose epitope is on the HSV-1 gD portion of the gDCD4T molecule) to glyceryl coated controlled pore glass by the method of Roy et al., 1984. The concentrated cell culture fluid is applied directly to the column and the contaminating proteins are washed away with neutral pH buffer. The column is then washed with neutral buffer containing tetramethylammonium chloride followed by neutral buffer containing Tween 80. The bound gDCD4T is eluted from the column with buffer at pH3 containing Tween 80 (0.1% w/v) and is neutralized immediately as it is eluted. The eluted neutralized

-44-

gDCD4T is then concentrated by ultrafiltration and dialyzed/diafiltered to exchange the buffer for a physiological salt solution containing Tween 80 at approximately 0.1% w/v.

5 If the detergent is not present the gDCD4T forms aggregates as evidenced by the ability of centrifugation at approximately 10,000 Xg for 2 minutes to remove the gDCD4T from the solution. Incubation of gDCD4T at 4°C in 0.1M sodium acetate, 0.5M NaCl and 0.25M tris at pH 7 together with BSA, Tween 80 or glycerol as
10 candidate stabilizers showed that, in the absence of a stabilizer the gDCD4T gradually aggregated over the space of 12 days to the point where only about 60-70% of the protein was soluble. However, use of 0.1% w/v Tween 80 or (0.5 mg/ml BSA ensured that about 100% or 80%, respectively, of the gDCD4T remained soluble over this
15 period. Surprisingly glycerol was ineffective as a stabilizer and produced results inferior even to the control-at 8 days about 80% of the gDCD4T was aggregated when stored in the presence of glycerol.

20 Example 4

Plasmids were constructed to direct the expression of proteins containing differing lengths of the amino-terminal, extracellular domain of CD4 fused to the constant region of human immunoglobulin $\gamma 1$. These plasmids are referred to as pRKCD4 $\gamma 1$,
25 pRKCD4 $\gamma 1$, pRKCD4 $\gamma 1$, pRKCD4 $\gamma 1$, and pRKCD4 $\gamma 1$.

Plasmid pRKCD4 $\gamma 1$ contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for serine residue 366 of the mature CD4 polypeptide, immediately followed by
30 the sequence coding for the constant region of human immunoglobulin $\gamma 1$, starting at the codon for serine residue 114 of mature human immunoglobulin $\gamma 1$ (Kabat et al.).

Plasmid pRKCD4 $\gamma 1$ contains the portion of the CD4 gene
35 from the initiation codon to the fusion site after the codon for

-45-

lysine residue 360 of the mature CD4 polypeptide, immediately followed by the sequence coding for the constant region of human immunoglobulin γ 1, starting at the codon for serine residue 114 of mature human immunoglobulin γ 1 (Kabat et al.).

5

Plasmid pRKCD4₂ γ 1 contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for glutamine residue 180 of the mature CD4 polypeptide, immediately followed by the sequence coding for the constant region of human immunoglobulin γ 1, starting at the codon for serine residue 114 of mature human immunoglobulin γ 1 (Kabat et al.).

10

Plasmid pRKCD4_{e2} γ 1 contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for leucine residue 177 of the mature CD4 polypeptide, immediately followed by the sequence coding for the constant region of human immunoglobulin γ 1, starting at the codon for serine residue 114 of mature human immunoglobulin γ 1 (Kabat et al.).

15

Plasmid pRKCD4₁ γ 1 contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for aspartic acid residue 105 of the mature CD4 polypeptide, immediately followed by the sequence coding for the constant region of human immunoglobulin γ 1, starting at the codon for serine residue 114 of mature human immunoglobulin γ 1 (Kabat et al.).

20

25

Plasmid pRKCD4_{e1} γ 1 contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for leucine residue 100 of the mature CD4 polypeptide, immediately followed by the sequence coding for the constant region of human immunoglobulin γ 1, starting at the codon for serine residue 114 of mature human immunoglobulin γ 1 (Kabat et al.).

30

-46-

Construction of these plasmids required the prior construction of plasmid pRKCD4TP/γ1. It was constructed as follows:

5 A cDNA clone coding for human immunoglobulin γ1 was obtained from a human spleen cDNA library (Clontech Laboratories, Inc.) using oligonucleotides based on the published sequence (Ellison et al., "Nucl. Acids Res." 10:4071-4079 [1982]), and an EcoRI-EagI fragment (the EcoRI site was contributed by a linker; 10 see Fig. 4a,b) containing part of the variable and all of the constant region was obtained. This fragment was blunted with Klenow fragment, and recovered by gel electrophoresis (Fragment al).

15 Plasmid pRKCD4TP-kk, encoding a substitutional variant of soluble CD4 (residues 1-368) containing a lysine residue instead of asparagine at position 1 of the mature polypeptide, was constructed from plasmid pRKCD4TP by site-directed mutagenesis. A synthetic oligonucleotide was made as a primer for a mutagenesis reaction to 20 obtain the desired coding sequence. This was synthesized as a 51-mer which contained two silent mutations from the natural sequence in addition to the substitution mutation, and 21 bases on each side of the mutated codons:

5'- CCC TTT TTT GCC CAG CAC CAC CTT CTT GCC CTG-
25 AGT GGC TGC TGC GAG GAG -3'

Plasmid pRKCD4TP was transformed into *E. coli* strain SR101 and the transformed colonies plated on ampicillin media plates. Resistant colonies were selected and grown in the presence of 30 m13K07 helper bacteriophage to yield secreted, encapsidated single-stranded templates of pRKCD4TP. The single-stranded plasmid DNA was isolated and used as the template for mutagenesis reactions with the synthetic oligonucleotides described above as primers. The mutagenesis reaction was transformed *E. coli* SR101 and the 35 transformed culture plated on ampicillin media plates.

-47-

Transformants were screened by colony hybridization (ref. Grunstein-Hogness) for the presence of the appropriate sequence, using the following 16 mer as the probe.

5'- C CAC CTT CTT GCC CTG -3'

5 The hybridization conditions chosen were sufficiently stringent that the probe only detects the correctly fused product. Colonies identified as positive were selected and plasmid DNA was isolated and transformed into *E. coli* strain SR101. The transformed cultures were plated on ampicillin media plates, and resistant colonies were selected and grown in the presence of m13K07 bacteriophage. Templates were prepared as above and screened by sequencing.

15 Plasmid pRKCD4TP-kk was digested with XbaI and treated with Klenow Enzyme, and Fragment a2, containing the linearized plasmid was recovered by gel electrophoresis, and ligated with fragment a1. The ligation mixture was transformed into *E. coli* strain 294, the transformed culture plated on ampicillin media plates and resistant colonies selected. Plasmid DNA was prepared from the transformants and checked by restriction analysis for the presence of the correct fragment in the correct orientation (i.e., the immunoglobulin coding region in the same orientation as the CD4 coding region, and at the 3' end of the CD4 coding region). This plasmid is referred to as pRKCD4TP/γ1.

25 Synthetic oligonucleotides were made as primers for deletional mutagenesis reactions to fuse the appropriate coding sequences of IgG1 and CD4 as described above. These were synthesized as 48-mers comprising 24 nucleotides on each side of the desired fusion site (i.e., corresponding to the COOH-terminal 8 residues of the desired CD4 moiety, and the NH₂-terminal 8 residues of the desired immunoglobulin moiety). Plasmid pRKCD4TP/γ1 was transformed into *E. coli* strain SR101 and the transformed cultures plated on ampicillin media plates. Resistant colonies were selected and grown in the presence of m13K07 helper bacteriophage

-48-

to yield secreted, encapsidated single-stranded templates of
PRKCD4TP/γ1. The single-stranded plasmid DNA was isolated and used
as the template for mutagenesis reactions with the synthetic
oligonucleotides described above as primers. The mutagenesis
5 reactions were transformed *E. coli* SR101 and the transformed
culture plated on ampicillin media plates. Transformants were
screened by colony hybridization (ref. Grunstein-Hogness) for the
presence of the appropriate fusion site, using 16mers as probes.
These 16mers comprise 8 bases on either side of the fusion site,
10 and the hybridization conditions chosen were sufficiently stringent
that the probes only detect the correctly fused product. Colonies
identified as positive were selected and plasmid DNA was isolated
and transformed into *E. coli* strain SR101. The transformed
cultures were plated on ampicillin media plates, and resistant
15 colonies were selected and grown in the presence of m13K07
bacteriophage. Templates were prepared as above and screened by
sequencing.

The plasmids were transfected into 293 cells using standard
20 procedures and assayed for expression and production as described
above.

	<u>Expressed</u>	<u>Secreted</u>
PRKCD4 ₁ γ1	+	-
25 PRKCD4 ₂ γ1	+	+
PRKCD4 ₂ γ1	+	+
PRKCD4 ₄ γ1	+	+
PRKCD4 ₄ γ1	+	+

30 Plasmids also were constructed to direct the expression of
fusion proteins containing differing lengths of the amino-terminal,
extracellular domain of CD4 fused to the truncated portion of the
constant region of human immunoglobulin γ1, comprising only the
hinge region and constant domains CH₂ and CH₃.

35

Synthetic oligonucleotides were made as primers for mutagenesis reactions to delete the immunoglobulin sequence from Ser114 to Cys215 inclusive (Kabat et al.). These were synthesized as 48-mers comprising 24 nucleotides on each side of the desired fusion site (i.e., corresponding to the COOH-terminal 8 residues of the desired CD4 moiety, and the NH₂-terminal 8 residues of the desired immunoglobulin moiety). Plasmids pRKCD₄₋₁, pRKCD₄₋₂ and pRKCD₄₋₁ were separately transformed into E. coli strain SR101 and the transformed culture plated on ampicillin media plates. Resistant colonies were selected and grown in the presence of m13K07 helper bacteriophage to yield secreted, encapsidated single-stranded templates of these plasmids. The single-stranded plasmid DNA was isolated and used as the template for mutagenesis reactions with the synthetic oligonucleotides described above as primers. The mutagenesis reactions were transformed E. coli SR101 and the transformed culture plated on ampicillin media plates. Transformants were screened by colony hybridization (Grunstein-Hogness) for the presence of the appropriate fusion site, using 16mers as probes. These 16mers comprise 8 bases on either side of the fusion site, and the hybridization conditions chosen were sufficiently stringent that the probes only detect the correctly fused product. Colonies identified as positive were selected and plasmid DNA was isolated and transformed into E. coli strain SR101. The transformed cultures were plated on ampicillin media plates, and resistant colonies were selected and grown in the presence of m13K07 bacteriophage. Templates were prepared as above and screened by sequencing.

The plasmid derived from plasmid pRKCD₄₋₁ is referred to as pRKCD₄Fc1, that derived from plasmid pRKCD₄₋₂ is referred to as pRKCD₂Fc1 and that derived from plasmid pRKCD₄₋₁ is referred to as pRKCD₄Fc1.

-50-

pRKCD4₂Fc1, pRKCD4₁Fc1 and pRKCD4₄Fc1 are cultured in the same fashion as described above and CH1-deleted CD4 immunoadhesons recovered as described elsewhere herein.

5 Light Chain Fusions

Plasmids were constructed to direct the expression of proteins containing differing lengths of the amino terminal, extracellular domain of CD4 fused to the constant region of human immunoglobulin κ . These plasmids are referred to as pRKCD4_{4 κ} and pRKCD4_{6 κ} .

10 Plasmid pRKCD4_{4 κ} contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for serine residue 366 of the mature CD4 polypeptide, immediately followed by the sequence for the constant region of human immunoglobulin κ , starting at the codon for threonine residue 109 of the mature human immunoglobulin κ . (Kabat et al.)

20 Plasmid pRKCD4_{6 κ} contains the portion of the CD4 gene from the initiation codon to the fusion site after the codon for lysine residue 360 of the mature CD4 polypeptide, immediately followed by the sequence for the constant region of human immunoglobulin κ , starting at the codon for threonine residue 109 of the mature human immunoglobulin κ . (Kabat et al.)

25 These plasmids were constructed in a manner analogous to plasmids pRKCD4_{4 γ 1} and pRKCD4_{6 γ 1} described above, with the following exception:

30 The human immunoglobulin κ coding sequence (Fig. 5) was obtained from a human spleen cDNA library (Clontech Laboratories, Inc.) using oligonucleotides based on the published sequence (Hieter, P.A. et al., Cell 22:197-207 [1980]) and an EcoRI-BspMI fragment containing part of the variable region and the entire constant region was obtained (see Fig. 5). This fragment was

35

-51-

blunted with Klenow fragment and the four dNTPs. This fragment was used instead of fragment a1, and was used to construct plasmid pRKCD4TP/hc.

5 Expression in CHO Cells

Plasmids were or are constructed to direct the expression of the immunoadhesons described above in CHO cells. These are referred to as pSVeCD4_{γ1}SVDHFR, pSVeCD4_{2γ1}SVDHFR, pSVeCD4_{1γ1}SVDHFR, pSVeCD4_{e4γ1}SVDHFR, pSVeCD4_{e2γ1}SVDHFR, pSVeCD4_{e1γ1}SVDHFR, pSVeCD4_{4Fc1}SVDHFR, pSVeCD4_{2Fc1}SVDHFR, pSVeCD4_{1Fc1}SVDHFR, pSVeCD4_{4κ}SVDHFR and pSVeCD4_{2κ}SVDHFR.

Fragment 31 was prepared as described above. Fragment 32a was prepared by digesting plasmid pE348HBV.E400 D22 with BamHI, blunting with Klenow fragment and the four dNTPs, then digesting with PvuII and isolating the large fragment containing the balance of the β-lactamase gene and the SV40 early promoter and the DHFR gene. Plasmids pRKCD4_{γ1}, pRKCD4_{2γ1}, pRKCD4_{1γ1}, pRKCD4_{e4γ1}, pRKCD4_{e2γ1}, pRKCD4_{e1γ1}, pRKCD4_{4Fc1}, pRKCD4_{2Fc1}, pRKCD4_{1Fc1}, pRKCD4_{4κ} and pRKCD4_{2κ} were separately digested with HindIII, blunted with Klenow fragment and the four dNTPs, then digested with EcoRI and the fragments encoding the CD4-Ig fusion protein were isolated. The resulting DNA fragments were ligated together with fragments 31 and 32a and transformed into *E. coli* strain 294. Colonies were selected and checked for the presence of the correct plasmid as above, then transfected into CHO cells and amplified by methotrexate selection using conventional procedures.

30 Example 5

30 Culture, Purification and formulation of CD4 variants

Plasmids encoding soluble CD4 adhesons such as CD4T, CD4TP, or soluble CD4 immunoadhesons were calcium phosphate transfected into CHO-DP7 (a proinsulin-transformed autocrine host cell derived from CHO; U.S.S.N. 97,472) and the transformants grown in selective

-52-

medium (1:1 HAM F12/DMEM GHT⁺ containing 1 - 10% diafiltered or dialyzed bovine serum). Other suitable host cells are CHO cells or 293S human embryonic kidney cells. The transformants were amplified by methotrexate selection in the same medium but containing 500 nm methotrexate. A subclone capable of secreting CD4TP. CD4tp 500 b. was selected. CD4tp 500 b is cultured in a DMEM/HAM F12 medium at about 37°C until CD4TP accumulates in the culture, after which the medium is separated from the cells and insoluble matter by centrifuging.

Culture fluid from CD4TP transformants was concentrated and diafiltered to lower the ionic strength. The concentrate was passed through a large volume of Q-Sepharose anion exchange resin (previously equilibrated with 25 mM NaCl, pH 8.5) in order to adsorb contaminants from the culture fluid. The isoelectric point of CD4TP is about 9.5, thus making it possible to discriminate between truncated forms of CD4 and most contaminants by alternate adsorption, respectively, on a cation exchange resin such as carboxymethyl or sulfonyl Sepharose, and an anion exchange resin such as quaternary ammonium Sepharose. In addition, since highly electropositive domains are present in the extracellular segment of CD4 any CD4-containing variant is purified in the same fashion as CD4TP. The unadsorbed culture fluid from the anion exchange resin step was then passed through a cation exchange resin (previously equilibrated with 25 mM NaCl at pH 8.5) whereby CD4TP was adsorbed to the resin. The CD4TP was eluted with a NaCl gradient at pH 8.5, this CD4 variant eluting at about 0.2 M NaCl. Ammonium sulfate was added to the eluate to a concentration of 1.7M and the solution passed through a column of hydrophobic interaction chromatography resin (phenyl or butyl Sepharose). The CD4TP was eluted from the hydrophobic interaction column with a gradient of ammonium sulfate, the CD4TP emerging at about 0.7M ammonium sulfate. The eluate was concentrated and buffer exchanged on a G-25 column using phosphate buffered saline containing .02 % (w/v) Tween 20 or Tween 80. The CD4TP was soluble and stable in this solution, which was sterile

-53-

filtered and filled into vials as an aqueous formulation. Other polymeric nonionic surfactants are suitably used with the CD4 formulations, including Pluronic block copolymers or polyethylene glycol.

5

It is also possible to employ immunoaffinity purification of soluble CD4 wherein the CD4 is adsorbed onto an immobilized antibody against CD4. This method suffers from the disadvantage that elution of the soluble CD4 under acidic conditions leads to protein aggregation that is only thoroughly ameliorated at relatively higher levels of surfactant. The foregoing procedure permits the use of much lower quantities of surfactant, about from 0.01 to 0.10 % (w/v) surfactant.

10

15

The procedure followed for the purification of CD4 fusions with immunoglobulin heavy chain was to concentrate recombinant supernatants by ultrafiltration and thereafter adsorb the fusion onto resin-immobilized Staphylococcal protein A. The fusion was eluted with 0.1M citrate buffer pH 3 with no salt or detergent. This preparation is buffered into Tris buffer at pH 7.5. The immunoglobulin fusions with CD4 V1-V4 optionally are further purified by the procedure described above for unfused CD4 variants. CD4 immunoglobulin fusions with CD4 V1-V2 also may be purified by the procedure above, except that it is not expected that the isoelectric point of this class of molecules will be as alkaline as that of species containing all four V regions of CD4.

20

25

Example 6

The characteristics of several adhesion variants were determined. As shown in table 4 the immunoadhesions CD4_{4γ1} and CD4_{2γ1} show improved plasma half-life in rabbits, coupled with high-affinity gp120 binding and an affinity for Fcγ receptor (determined with U937 cells) that is comparable to that of bulk human IgG1.

30

35

-54-

Table 4

gp120 KD (nM)*		FcγR KD (nM)+	Plasma Half-Life++ In Rabbits (Hrs.)
5	CD4T ^s	Not detected	0.25
	CD4 _{4γ1}	2.83 ± 0.25	6.4
10	CD4 _{2γ1}	3.01 ± 0.68	40.6
	human IgG1	3.52 ± 0.5	21 days*

* determined in humans

+ KD was determined by the method of Anderson et al., "J. Immunol." 125:2735-2741 (1980).

* determined by the method of Smith et al., "Science" 238:1704-07 (1987).

§ residues 1-368 only

++ The adheson variant was injected intravenously into rabbits and samples of blood were collected periodically and assayed for the presence of the adheson variant.

** Not done.

Claims:

1. Nucleic acid encoding an amino acid sequence variant of an adhesion.
- 5 2. The nucleic acid of claim 1 wherein the adhesion is a CD4 polypeptide.
3. The nucleic acid of claim 2 wherein the variant is a CD4 polypeptide in which nucleic acid encoding the transmembrane domain has been modified whereby the CD4 polypeptide encoded
10 thereby contains an inactivated transmembrane domain.
4. The nucleic acid of claim 3 wherein the transmembrane domain has been inactivated by its deletion or by substituting for
15 the transmembrane domain an amino acid sequence having a substantially hydrophilic hydropathy profile.
5. The nucleic acid of claim 2 wherein the variant comprises a fusion of (a) a polypeptide different from the CD4 and (b) a
20 CD4 polypeptide.
6. The nucleic acid of claim 5 wherein the polypeptide different from the CD4 bears a non-CD4 immune epitope.
- 25 7. The nucleic acid of claim 6 wherein the polypeptide different from CD4 is fused to the amino or carboxyl terminus of mature CD4 and the transmembrane domain of CD4 has been inactivated.
8. The nucleic acid of claim 5 wherein the different polypeptide
30 comprises a signal sequence.
9. The nucleic acid of claim 5 wherein the different polypeptide contains about from 5 to 1000 residues.

-56-

10. The nucleic acid of claim 9 wherein the different polypeptide is capable of eliciting a humoral immune response in an animal.
- 5 11. The nucleic acid of claim 10 wherein the different polypeptide is a viral polypeptide or an allergen.
12. The nucleic acid of claim 5 wherein the different polypeptide is a human plasma protein having a plasma half life greater than from which the transmembrane domain has been deleted.
- 10 13. The nucleic acid of claim 12 wherein the variant is a fusion of a polypeptide comprising at least one V-like domain of CD4 fused with a polypeptide comprising an immunoglobulin constant domain.
- 15 14. The nucleic acid of claim 1 wherein the adhesion is CD4, CD8 or the high affinity IgE receptor.
- 20 15. The nucleic acid of claim 2 wherein the variant consists essentially of the V₁ through V₄ or V₁ through V₂ regions of the CD4 antigen.
- 25 16. The nucleic acid of claim 2 which consists essentially of the CD4 insert of pCD4AN1a.
17. The nucleic acid of claim 12 wherein the different polypeptide is albumin, apolipoprotein or transferrin.
- 30 18. The nucleic acid of claim 8 wherein the signal sequence is a bacterial signal sequence.
19. The nucleic acid of claim 15 wherein the variant consists essentially of CD4 residues 1-368.

35

-57-

20. The nucleic acid of claim 15 wherein the variant consists essentially of CD4 residues 1-180.
21. The nucleic acid of claim 13 wherein the immunoglobulin constant domain is the constant domain of an IgG heavy chain.
22. The nucleic acid of claim 5 wherein the different polypeptide is a cytotoxic polypeptide.
23. The nucleic acid of claim 5 wherein the cytotoxic polypeptide is the diphtheria toxin A.
24. A composition comprising an adhesion amino acid sequence variant which is incapable of cell membrane anchorage.
25. The composition of claim 24 wherein the adhesion variant comprises a CD4 amino acid sequence capable of binding gp120.
26. The composition of claim 25 further comprising an agent for inhibiting the aggregation of the variant selected from the group of a predetermined protein and a surfactant.
27. The composition of claim 26 wherein the agent is a surfactant.
28. The composition of claim 27 wherein the surfactant is Tween 80 or Tween 20.
29. The composition of claim 25 wherein the CD4 transmembrane domain has been deleted or has been substituted for by an amino acid sequence having a substantially hydrophilic hydropathy profile.
30. The composition of claim 29 which is sterile and which further comprises a physiologically acceptable carrier.

31. The composition of claim 25 wherein the variant comprises an immunoglobulin amino acid sequence.
- 5 32. The composition of claim 31 wherein the immunoglobulin sequence comprises a constant domain sequence of an immunoglobulin heavy chain.
- 10 33. The composition of claim 32 wherein the constant domain is linked at its N-terminus to the C-terminus of a transmembrane-deleted CD4 polypeptide.
34. The composition of claim 33 wherein the CD4 polypeptide contains V_1V_2 .
- 15 35. The composition of claim 33 wherein the CD4 polypeptide contains $V_1V_2V_3V_4$.
36. The composition of claim 31 wherein the variant is in the form of a dimer.
- 20 37. The composition of claim 36 wherein the composition comprises a fusion of a CD4 V-like domain to an immunoglobulin heavy chain constant domain.
- 25 38. The composition of claim 31 wherein the variant is selected from the group consisting of
- (a) AC_L ;
- (b) AC_L-AC_L ;
- 30 (c) $AC_H-[AC_H, AC_L-AC_H, AC_L-V_HC_H, V_LC_L-AC_H, \text{ or } V_LC_L-V_HC_H]$;
- (d) $AC_L-AC_H-[AC_H, AC_L-AC_H, AC_L-V_HC_H, V_LC_L-AC_H, \text{ or } V_LC_L-V_HC_H]$;
- (e) $AC_L-V_HC_H-[AC_H, AC_L-AC_H, AC_L-V_HC_H, V_LC_L-AC_H, \text{ or } V_LC_L-V_HC_H]$;
- (f) $V_LC_L-AC_H-[AC_H, AC_L-AC_H, AC_L-V_HC_H, V_LC_L-AC_H, \text{ or } V_LC_L-V_HC_H]$;
- or
- 35 (g) $[A-Y]_n-[V_LC_L-V_HC_H]_2$

-59-

wherein A is a CD4 polypeptide containing a CD4 variable region-like domain; V_L , V_H , C_L and C_H represent light or heavy chain variable or constant domains of an immunoglobulin; n is an integer; and Y designates the residue of a covalent cross-linking agent.

39. The composition of claim 38 wherein the V_L and V_H domains are capable of binding a predetermined antigen.
- 10 40. The composition of claim 31 wherein the immunoglobulin sequence is obtained from IgG1, IgG2, IgG3, IgG4, IgA, IgE, IgD or IgM.
- 15 41. The composition of claim 25 wherein the variant comprises a polypeptide different from CD4 which is nonimmunogenic in humans.
- 20 42. The composition of claim 41 wherein the variant comprises a polypeptide which is immunogenic in humans.
- 25 43. The composition of claim 41 wherein the variant comprises a polypeptide having a human plasma half life which is greater than about 20 hours.
44. The composition of claim 41 wherein the variant comprises a human transferrin, apolipoprotein or albumin polypeptide.
45. The composition of claim 25 wherein the variant comprises a cytotoxic polypeptide.
- 30 46. The composition of claim 45 wherein the cytotoxic polypeptide is ricin A chain or diphtheria toxin A.
- 35 47. A polypeptide comprising a CD4 amino acid sequence capable of binding gp120 which is cross-linked to (a) polypeptide having

-60-

a plasma half life of greater than about 20 hours or (b) a cytotoxic polypeptide.

- 5 48. The polypeptide of claim 47 wherein the polypeptide of (a) is transferrin, an apolipoprotein or albumin.
49. The polypeptide of claim 47 wherein the cytotoxic polypeptide is cross-linked to the CD4 variable-like domain by a bifunctional cross-linking agent.
- 10 50. A method for preparing an adhesion variant comprising transfecting a host cell with the nucleic acid of claim 1.
51. A method for preparing an adhesion variant comprising
15 recovering the variant from the culture of a host cell transfected with the nucleic acid of claim 1.
52. The method of claim 51 wherein the adhesion is CD4 and the variant is recovered from the culture medium of the host cell
20 or from the cell itself.
53. The method of claim 52 wherein the variant is recovered by adsorption onto a cation exchange resin.
- 25 54. The method of claim 53 wherein the variant is recovered by adsorption of contaminants onto an anion exchange resin.
55. The method of claim 52 wherein the variant lacks a functional transmembrane domain.
- 30 56. The method of claim 52 wherein wherein a salt is added to the culture medium to occupy charged domains of the variant, the resulting solution is contacted with a hydrophobic affinity chromatography resin to adsorb the variant, and the variant

-61-

eluted from the resin by washing the resin with a declining gradient of salt.

- 5 57. The method of claim 52 wherein the variant is recovered by immunoaffinity chromatography.
58. The method of claim 57 wherein the immunoaffinity chromatography is directed against a polypeptide different from CD4 which is fused to CD4.
- 10 59. A method for the treatment of an HIV infection comprising administering to a patient infected with HIV a therapeutically effective dose of an amino acid sequence variant of CD4.
- 15 60. A replicable vector comprising the nucleic acid of claim 1.

FIG. 1A

[illegible]

2/13

FIG. 1B-I

601 *GGAGCTCCAGGATAGTGGACCTGGACATGCTTGCAGAACCAAGAGGTGGAGTTCMAAATAGACATCCTGGTGCTAGCTTTCCAGAGGCC*
 CCTCAGGTCCTATCACCTGGACCTGTACGTGACAGAACGCTTTGGTCTTCTCCACCTCAAGTTTATCTGTAGCACCAACGATCGAAAGGTCTTCGGG
 GluLeuGlnAspSerGlyThrTrpThrCysThrValLeuGlnAsnGlnLysLysValGluPheLysAlaAspIleValValLeuAlaPheGlnLysAla
 150 *GGAGCTCCAGGATAGTGGACCTGGACATGCTTGCAGAACCAAGAGGTGGAGTTCMAAATAGACATCCTGGTGCTAGCTTTCCAGAGGCC*
 TCCAGCATAGCTATAGAAAGAGGGGGACAGGTGGAGTCTCTCCCACTCGCTTTACAGTTGMAAGCTGACGGGCACCTGGCGAGCTGTGGTGGC
 AGTCGTATCAGATATCTTCTCCCTTGTCCACCTCAAGAGGAGGTGACGGGAATGTCAACTTTTCGACTGCCCTGACCGCTCGACACCCACCG
 183 SerSerIleValTyrLysLysGluGlyGluGlnValGluPheSerPheProLeuAlaPheThrValGluLysLeuThrGlySerGlyGluLeuTrpTrpGln
 801 *AGGCGGAGAGGGCTTCTCTCCAGCTTGGATCACCTTGGACCTGAAAGAACAGGAGTGTCTGTAAACGGGTACCCAGGACCTTAAGCTCCAGAT*
 TCCGCTCTCCCGAAGAGGAGGTTCAGAACTAGTGGAACTGGACTCTTGTCTTCACAGACATTTGCCCAATGGGTCTCTGGGATTCGAGTCTA
 217 AlaGluArgAlaSerSerSerLysSerTrpIleThrPheAspLeuLysAsnLysGluValSerValLysArgValThrGlnAspProLysLeuGlnMet
 701 *TCCAGCATAGCTATAGAAAGAGGGGGACAGGTGGAGTCTCTCCCACTCGCTTTACAGTTGMAAGCTGACGGGCACCTGGCGAGCTGTGGTGGC*
 AGTCGTATCAGATATCTTCTCCCTTGTCCACCTCAAGAGGAGGTGACGGGAATGTCAACTTTTCGACTGCCCTGACCGCTCGACACCCACCG
 183 SerSerIleValTyrLysLysGluGlyGluGlnValGluPheSerPheProLeuAlaPheThrValGluLysLeuThrGlySerGlyGluLeuTrpTrpGln
 801 *AGGCGGAGAGGGCTTCTCTCCAGCTTGGATCACCTTGGACCTGAAAGAACAGGAGTGTCTGTAAACGGGTACCCAGGACCTTAAGCTCCAGAT*
 TCCGCTCTCCCGAAGAGGAGGTTCAGAACTAGTGGAACTGGACTCTTGTCTTCACAGACATTTGCCCAATGGGTCTCTGGGATTCGAGTCTA
 217 AlaGluArgAlaSerSerSerLysSerTrpIleThrPheAspLeuLysAsnLysGluValSerValLysArgValThrGlnAspProLysLeuGlnMet

3/13

```

          haeIII          sau96I
          stul            scrFI
          haeI            bphI  haeIII
                        mnlI  bstNI
                        ddel
          aluI            901  GGCAAGAGCTCCCGCTCCACCTCACCTGCCCCAGGCTTGCTCAGTATGCTGGCTCTCGAAGCTCACCCCTGCCCCTTGAGCGGAACAGCAAG
          mnlI  ecoNI  bstNI  mnlI  ddel
          bphI  scrFI  ddel
          250  GlyLysLeuProLeuHisLeuThrLeuProGlnAlaLeuProGlnTyrAlaGlySerGlyAsnLeuThrLeuAlaLeuGluAlaLysThrGlyLys
          aluI            sau96I
          scrFI  bstNI  hphI  aluI  ddel
          bstNI  hphI  ddel
          sfaNI  1001  TTGCATCAGGAAGTGAACTCGTGTGATGAGAGCCACTCAGCTCAGAAAATTGACCTGTGAGGTGTGGGACCCACCTCCCTTAAGCTGATGCTGA
          AACGTAGTCTTCACTTGGACCACTACTCTCGGTGAGTCGAGGTCTTTTAACTGGACACTCCACACCCCTGGTGGAGGGGATTCGACTACGACT
          283  LeuHisGlnGluValAsnLeuValValMetArgAlaThrGlnLeuGlnLysAsnLeuThrCysGluValTyrGlyProThrSerProLysLeuMetLeuSer
          mnlI  ddel
          mstII  foki  aluNI  ddel  pfi
          ecoRI  1101  GTTTGAACCTGGAGAACAGGAGGCAAGGTCTCGAAGCGGGAGAGCGCGTGTGGGTGCTGAAACCTGAGCGGGGATGTGGCAGTGTCTGCTGAGTGA
          CAACTTTGACCTCTGTCTCCGTTTCCAGAGCTTCGCCCTCTTCGCCCAACCCACGACTTGGGACTCCGCCCTTACACCGTCACAGACGACTCACT
          317  LeuLysLeuGluAsnLysGluAlaLysValSerLysArgGluLysAlaValTyrValLeuAsnProGluAlaGlyMetTyrGlnCysLeuLeuSerAsp

```

FIG. 1B-2

[illegible]

FIG. 1C

[illegible]

FIG. 2B-1

[illegible]

	haeIII	sau96I	
	stui	scrFI	
	bael	hphI haeIII	
	scrFI	nmlI batNI ddeI	
	hphI	nmlI	
	nmlI ecoNI batNI		
	alul		
1001	AGTCCCGGTCCACCTCACCTGCCCCAGGCCCTGCCTCAGTAGTGCTGGCTCTGGAAACCTCACCTGGCCCTTGAGCGGAACAACAGGAAAGTTGCATCA		sfaNI
	TCGAGGGCGAGGTGGAGTGGACGGGTCCGGAACGGAGTCATACGACCAGAACCTTTGGAGTGGACCGGAACCTTCGCTTTTGCTTTCACACGTAGT		
	LeuProLeuHISLeuthrLeuProGlnAlaLeuProGlnTyraLeuGlySerGlyAsnLeuthrLeuAlaLeuGlualaLysThrGlyLysLeuHisGln		
310		sau96I	
		nlaIV	
		avaII	
		ppuMI	
		nlaIV	
	alul	nmlI	alul ddeI
	ddeI	ecoO	
	scrFI		
	batNI hphI		
1101	GGAAGTGAACCTTGCTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTGACTGTGAGGTGTGGGAGCCCACCTCCCTTAAGCTGATGCTGAGTTTGAAA		
	CCTTCACCTGGACCACCACTACTCTCGTGAGTTCGAGGTCTTTTAACTTGACACTCCACACCTCGGTGGAGGGGATTCGACTACGACTCAAACTTT		
343	GluValAsnLeuValMetArgAlaThrGlnLeuGlnLysAsnLeuthrCysGluValTrpGlyProthrSerProLysLeuMetLeuSerLeuLys		

FIG. 2B-2

8 / 13

```

          mliI      auaI      ptaI      hinfI      aluNI
          ddel      mstII      foki      aluNI      ddel      aluNI
          ecobII      foki      aluNI      ddel      aluNI
          taqI      mliI      auaI      ptaI      hinfI      aluNI
          1201 CTGGAGAACAGGAGGCAAGGTCTCGAAGCGGAGCAGCGGTGCTGAACCTCAGCGCGGGGATGTGGCAGTGTCTGCTGAGTCACTCGGGAC
          GACCTTGTTCTCCGTTCCAGAGCTTCGCCCTCTTCGCCACACCCAGCACTTGGGACTCCGCCCTACACCGTCACAGCAGTCACTGAGCCCTG
          376 LeuGluAsnLysGluAlaLysValSerLysArgGluLysAlaValTrpValLeuAsnProGluAlaGlyMetTrpGlnCysLeuLeuSerAspSerGlyGln

          sau96I      auaI      aluI      mliI      mliI      mliI
          avaiI      aluI      mliI      mliI      mliI
          ppuNI      hinfI      hinfI      hinfI      hinfI      hinfI
          1301 AGTCTCTGCTGGAATCCACATCAAGGTCTGCCACATGTCCACCCGAGCTTTAATCGGTAGTTTATCAGTTAATTCCTAACGCAGTCAGGCA
          TCCAGGACGACTTAGGTTGTAGTTCACAGAGCGGTGTACAGGTGGGCTCGAATTAACCCATCAATAGTCAATTAACGATTGCTCAGTCCCT
          410 ValLeuLeuGluSerAsnIleLysValLeuProThrTrpSerThrProSerPheAsnAlaValValTyrHisSerOC

          hinfI      hinfI      hinfI      hinfI      hinfI      hinfI
          hinfI      hinfI      hinfI      hinfI      hinfI      hinfI
          1401 CCGTGTATGAATCTAACAAATGCGGTCTCATCTGTCATCTCGGACCCCTGACCTGGATGCTGTAGGCATAGGCTTGTTGTTATGCCGGTACTGCGGGCTCT
          GCCACATAGTTTAGATTGTTACGGGATGACGATAGGAGCGGTGGCAGTGGGACCTACGACATCCGTATCCGAACCAATACGGCCCATGACGGCCCGGAGA

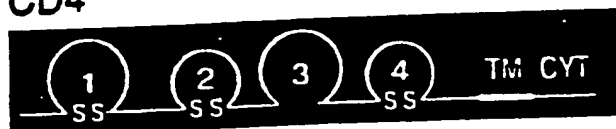
          1501 TCGCGGGAT
          ACGCCCTA

```

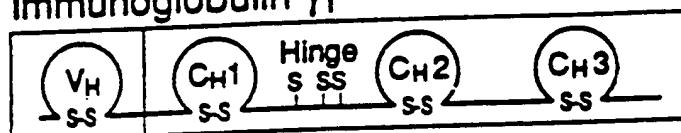
FIG. 2C

9/13

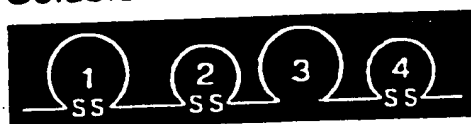
CD4



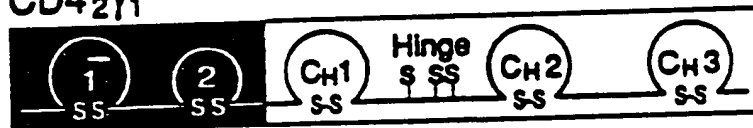
Immunoglobulin γ_1



Soluble rCD4



CD4 γ_1



CD4 γ_1

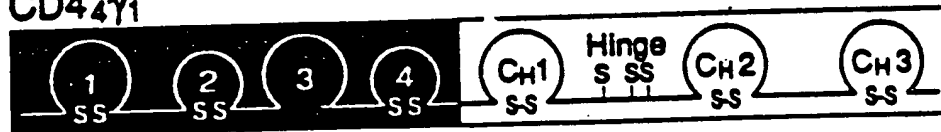


FIG. 3

10/13

FIG. 4A

1 GAAATCTGTCACTGCCGGGACACGGCCGTATATTACTGTGCGAGAGCCACCTTTTGGCTATGTTACAGGAGCGTCCCTTGTGGATCGACCCCTGG
 2 CTTAAGACAGTGCAGCGCGCTGTCCGGCATATAATGACAGCTCTCGGTGGAACAGATACCATGTCCCTCGCAGGGGGAACACCTAGCTGGGGACC
 3 ValThrAlaAlaAspThrAlaValTyrCysAlaArgAlaThrPheCysLeuTyrTyrArgGluArgProCysTyrPheAspTyrPhe
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000

11/13

FIG. 4B-1

[illegible]

[illegible]

13/13

sau96I
 avall
 nlaIV
 mnlI styl
 ecorI hphI
 fnu4HI bbvI mboII
 pstI haeIII
 fnu4HI bbvI
 haeIII
 1 GAATTCACCTTACCATCAGCGGCTGCAGCTGAAGATTTCGCACTTATTACTGCCAACAGTATAAGAGTTTGTGGCTCAGCTTCCGGCGGAGGACCA
 CTTAAGTCAGAGTGTAGTCGCGGACCTCGGACTTCTAAACAGTTGAATAGCTTGTATATTTCAAAACAGCGAGTGAAGCCGCTCCCTGCT
 ThrLeuThrIleSerGlyLeuGlnProGluAspPheAlaThrTyrcCysGlnGlnTyrcLysSerLeuSerLeuThrPheGlyGlyGlyThrLys
 72
 aaJAI fnu4HI mboII mnlI
 dplI bbvI
 101 AGGTGGAGATCAAAACGAACCTGTGGCTGCACCATCTGTCTTCACTTCCGCCCATCTGNTGACAGATTGAATCTGGAACCTGCCTCTGTTGTGCTGCTGCT
 TCCACCTCTAGTTGCTTGACACCGACCTGGTAGACAGAGTAGAAGCGGCTGACTACTCTCTCAACTTTAGACCTTGACGAGCAACACACAGGACGA
 104 ValGluIleLysArgThrValAlaAlaProSerValPheIlePheProSerAspGlnGlnLeuLysSerGlyThrAlaSerValValCysLeuLeu
 ← V K J K CK haeIII
 haeI
 xbaI mnlI
 201 GAATAACTTCTATCCACAGAGGCGCCAAAGTACAGTGAAGTGGTAAAGCCCTCCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACGCAAC
 CTTATGAAGTAGGGTCTCTCCGGTTTCATGTCACTTCCACCTTCCAGCTATTCGGGGAGGTAGCCCATTTAGGGTCTCTCACAGTGTCTGCTCTGCTGCTC
 137 AsnAsnPheTyrrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAspSerLys
 sacI
 hgiAI
 bsp1286
 haeIII
 sau96I aluI
 ecoO banII
 alwNI ddeI
 hphI
 301 GACAGCACCTACAGCCTCAGCAGCACCTGACGGCTGAGCAAAAGCAGACTACAGAAACACAAAGTCTACGGCTGCGAAGTACCCATCAGGCTGAGCT
 CTGTCGTGGATGTCGGAGTCGTCTGGGACTGCGACTGCTGCTGATCCTCTTGTGTTTCAATCGGACGCTTCAGTGGGTAGTCCCGGACTCGA
 170 AspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrrGluLysHisLysValTyrrAlaCysGluValThrHisGlnGlyLeuSerSer
 ddeI
 aluI
 401 CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGGGAGAGAGTGGCCCCACCTGCTCCTCAGT
 GCGGCGAGTGTTCGCAAGTTGTCCCTTCACANTCTCCCTCTTCACGGGGTGCGACGAGGAGTCA
 204 ProValThrLysSerPheAsnArgGlyGluCysAsn*

FIG. 5

INTERNATIONAL SEARCH REPORT

International Application No PCT/US 88/03414

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ¹ According to International Patent Classification (IPC) or to both National Classification and IPC IPC ⁴ : C 12 N 15/00; C 12 P 21/02; A 61 K 37/02; //G 01 N 33/566		
II. FIELDS SEARCHED Minimum Documentation Searched ⁷ Classification System: IPC ⁴ C 12 N; C 12 P; A 61 K Classification Symbols Documentation Searched other than Minimum Documentation to the extent that such documents are included in the Fields Searched ⁸		
III. DOCUMENTS CONSIDERED TO BE RELEVANT ⁹		
Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	Cell, vol. 42, no. 1, August 1985, P.J. Maddon et al.: "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family", pages 93-104, see figure 3, especially fragment T4B (cited in the application)	1-4,14-16, 19,20,24, 25,50-58,60
X	Proceedings of the National Academy of Sciences of the USA, vol. 84, March 1987 (US) S.J. Clark et al.: "Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: evidence for derivation from a structure with four immunoglobulin -related domains", pages 1649-1653, see figure 3	1,2,14,15, 60
X,P	WO, A, 88/01304 (THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK) 25 February 1988, see pages 69-75; examples 3-6	1-4,14-16, 19,20,24, 25,50-58,60
IV. CERTIFICATION Date of the Actual Completion of the International Search 21st December 1988 International Searching Authority EUROPEAN PATENT OFFICE Date of Mailing of this International Search Report 13. 01. 89 Signature of Authorized Officer P.C.G. VAN DER PUTTEN		

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET

X,P Science, vol. 238, 18 December 1987,
D.H. Smith et al.: "Blocking of HIV-1
infectivity by a soluble, secreted
form of the CD4 antigen", pages 1704-1707,
see the whole article

1-16,19,
24,25,29,
50-58,60

V. ☒ OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE

This international search report has not been established in respect of certain claims under Article 17(C) (a) for the following reasons:

1. ☒ Claim numbers 59 because they relate to subject matter not required to be searched by this Authority, namely:

please see Rule 39.1 (iv) - PCT:

Methods for treatment of the human or animal body by surgery
or therapy, as well as diagnostic methods.

2. ☐ Claim numbers because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim numbers because they are dependent claims and are not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

VI. ☐ OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This International Searching Authority found multiple inventions in this international application as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application.

2. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:

3. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:

4. ☐ As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remarks on Protest

- ☐ The additional search fees were accompanied by applicant's protest.
☐ No protest accompanied the payment of additional search fees.

ANNEX TO THE INTERNATIONAL SEARCH REPORT ON INTERNATIONAL PATENT APPLICATION NO.

US 8803414
SA -24961

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on 04/01/89
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A- 8801304	25-02-88	AU-A- 7879287 EP-A- 0280710	08-03-88 07-09-88
<hr/>			

EPD FORM 1079

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☒ **BLACK BORDERS**

☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

☐ **FADED TEXT OR DRAWING**

☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**

☐ **SKEWED/SLANTED IMAGES**

☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**

☐ **GRAY SCALE DOCUMENTS**

☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**

☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.